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(54) Title: COMPUTER BASED METHOD FOR PROTEIN ENGINEERING

(57) Abstract

The invention provides a computer based method and apparatus for identifying sites in a protein molecule which could be converted to cysteine residues to create a potentially protein-stabilizing disulfide bond. A central processing unit (102) is connected to a massbus (104) which connects the central processing unit (102) to storage devices (106, 108, 110, 112) which store the database containing the amino acid sequences and the application software package. A computer generated graphics system (116) receives images from the central processing unit (102) to be displayed. The display (120) allows an expert operator to view each potentially protein-stabilizing disulfide bond and rank them from most likely to stabilize an engineered protein to those least likely to stabilize the protein.

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TITLE OF THE INVENTION

COMPUTER BASED METHOD FOR PROTEIN ENGINEERING

BACKGROUND OF THE INVENTION

The present invention relates generally to a computer based method for designing molecules and more specifically to the use of this method to design more stable proteins.

1. Field of the Invention

The present invention provides a computer-assisted method for designing stable protein molecules.

2. Related Art

Proteins (or polypeptides) are linear polymers of amino acids. Since the polymerization reaction which produces a protein results in the loss of one molecule of water from each amino acid, proteins are often said to be composed of amino acid "residues." Natural protein molecules may contain as many as 20 different types of amino acid residues, each of which contains a distinctive side chain. The particular sequence of amino acid residues in a protein defines the primary sequence of the protein.

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Proteins fold into a three-dimensional structure. The folding is determined by the sequence of amino acids and by the protein's environment. The remarkable properties of proteins depend directly from the protein's three-dimensional conformation. Thus, this conformation determines the activity or stability of enzymes, the capacity and specificity of binding proteins, and the structural attributes of receptor molecules. Because the three-dimensional structure of a protein molecule is so significant, it has long been recognized that a means for stabilizing a protein's three-dimensional structure would be highly desirable.

The three-dimensional structure of a protein may be determined in a number of ways. Perhaps the best known way of determining protein structure involves the use of the technique of x-ray crystallography. An excellent general review of this technique can be found in *Physical Bio-chemistry*, Van Holde, K.E. (Prentice-Hall, NJ (1971) pp221-239) which reference is herein incorporated by reference. Using this technique, it is possible to elucidate three-dimensional structure with remarkable precision. It is also possible to probe the three-dimensional structure of a protein using circular dichroism, light scattering, or by measuring the absorption and emission of radiant energy (Van Holde, *Physical Biochemistry*, Prentice-Hall, NJ (1971)). Additionally, protein structure may be determined through the use of the techniques of neutron defraction, or by nuclear magnetic resonance (*Physical Chemistry*, 4th Ed. Moore, W.J., Prentice-Hall, NJ (1972) which reference is hereby incorporated by reference).

The examination of the three-dimensional structure of numerous natural proteins has revealed a number of

recurring patterns. Alpha helices, parallel beta sheets, and anti-parallel beta sheets are the most common patterns observed. An excellent description of such protein patterns is provided by Dickerson, R.E., et al. In: The Structure and Action of Proteins, W.A. Benjamin, Inc., CA (1969). The assignment of each amino acid to one of these patterns defines the secondary structure of the protein. The helices, sheets and turns of a protein's secondary structure pack together to produce the three-dimensional structure of the protein. The three-dimensional structure of many proteins may be characterized as having internal surfaces (directed away from the aqueous environment in which .the protein is normally found) and external surfaces (which are in close proximity to the aqueous environment). Through the study of many natural proteins, researchers have discovered that hydrophobic residues (such as tryptophan, phenylalanine, tyrosine, leucine, isoleucine, valine, or methionine) are most frequently found on the internal surface of protein molecules. In contrast, hydrophilic residues (such as asparate, asparagine, glutamate, glutamine, lysine, arginine, histidine, serine, threonine, glycine, and proline) are most frequently found on the external protein surface. The amino acids alanine, glycine, serine and threonine are encountered with equal frequency on both the internal and external protein surfaces.

Proteins exist in a dynamic equilibrium between a folded, ordered state and an unfolded, disordered state. This equilibrium in part reflects the interactions between the side chains of amino acid residues which tend to stabilize the protein's structure, and, on the

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other hand, those thermodynamic forces which tend to promote the randomization of the molecule.

The amino acid side chain interactions which promote protein folding and confer catalytic activity fall into two classes. The interactions may be caused by weak forces (e.g., hydrogen bonds) between the side chains of different amino acid residues. Alternatively, they may be caused by direct covalent bonding between the sulfhydryl groups of two cysteine amino acid residues. Such a bond is known as a "disulfide" bond.

When a protein is synthesized, any cysteine residues present contain free sulfhydryl groups (-SH). When two sulfhydryl groups in close proximity are mildly oxidized, disulfide bonds (-S--S-) may form, thereby crosslinking the polypeptide chain. The formation of this chemical bond is said to convert two "cysteine" residues into a "cystine" residue. Thus "cysteine" residues differ from a "cystine" residue in that the former molecules contain sulfur atoms which are covalently bonded to hydrogen, whereas the latter molecule contains a sulfur atom which is covalently bonded to a second sulfur atom.

A disulfide bond may stabilize the folded state of the protein relative to its unfolded state. The disulfide bond accomplishes such a stabilization by holding together the two cysteine residues in close proximity. Without the disulfide bond, these residues would be in close proximity in the unfolded state only a small fraction of the time. This restriction of the conformational entropy (disorder) of the unfolded state destabilizes the unfolded state and thus shifts the equilibrium to favor the folded state. The effect of the disulfide bond on the folded state is more difficult

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to predict.   It could increase, decrease or have no
effect on the free energy of the folded state.
Increasing the free energy of the folded state may lead
to a destabilization of the protein, which would tend to
cause unfolding.   Importantly, the cysteine residues
which participate in a disulfide bond need not be
located near to one another in a protein's primary amino
acid sequence.

One potential way of increasing the stability of a
protein is to introduce new disulfide bonds into that
protein.   Thus, one potential application of recombinant
DNA technology to the stabilization of proteins involves
the introduction of cysteine residues to produce
intraprotein disulfide bonds.   There are two ways in
which cysteine residues may be introduced into a
protein: (1) through a replacement-exchange with one of
the protein's normally occurring amino acid residues, or
(2) an insertion of a cysteine between two existing
amino acid residues.

Although the principles of recombinant DNA
technology permit the introduction of new cysteine
residues into a protein, they do not provide the
researcher with any suggestion of where the introduced
cysteine residues of the disulfide bond should be
placed, or which amino acid(s) should be exchanged by
such a replacement. Because of the substantial size and
complexity of protein molecules, an evaluation of
potential sites for disulfide bond linkages is
exceedingly complex.   Recently, investigators have
employed computers and computer graphics displays as an
aid for assessing the appropriateness of potential
linkage sites (Perry, L.J., & Wetzel, R., _Science_,
_226_:555-557 (1984); Pabo, C.O., _et al._, _Biochemistry_,

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25:5987-5991 (1986); Bott, R., et al., European Patent
Application Serial Number 130, 756; Perry, L.J., &
Wetzel, R., Biochemistry, 25:733-739 (1986); Wetzel,
R.B., European Patent Application Serial Number
155,832). The methods developed by Wetzel and
coworkers permit one to project the three-dimensional
conformation of a protein onto a computer screen and to
simulate the effect which a disulfide bond might have on
the protein's structure. Although these methods
facilitate the design of more stable proteins, the
researcher must still select the amino acid residues
which are to be replaced by the cysteine residues of the
disulfide bond. Hence, a substantial amount of guess
work and trial and error analysis are still required. A
need, therefore, still exists where a method which will
assist the user in selecting potential disulfide bond
linkage sites.

SUMMARY OF THE INVENTION

One goal of the present invention is to provide a
method for determining whether the active folded state
of a protein would be stabilized by the presence of a
disulfide bond between particular regions of the protein
molecule. The present invention accomplishes this goal
through the development of a novel computer based method
for selecting sites in natural proteins where the
introduction of a novel disulfide linkage will have a
high probability for stabilizing a particular protein.

In detail, the invention pertains to a computer
based method for evaluating a protein's structure to
determine whether the protein contains at least two
target amino acid residues, the replacement of at least

one of which with a cysteine residue would be sufficient to permit the formation of at least one potentially protein-stabilizing disulfide bridge; the method comprising the steps:

(1) examining each selected pair of amino acid residues in the protein to determine if they contain certain atoms whose relative three-dimensional positions possess a geometric conformation similar to the corresponding atoms of a known disulfide bridge,

(2) examining any pair of amino acids found to contain the certain atoms identified in step (1) to determine whether the new atoms of a possible disulfide linkage can be accommodated without creating unacceptable steric hindrance,

(3) permitting an expert operator (i) to view any possible sites for a novel disulfide linkage which can be accommodated without altering the tertiary conformation of the protein molecule, and (ii) to rank the viewed possible sites for a novel disulfide linkage from most likely to stabilize an engineered protein, to least likely to stabilize the protein, and

(4) evaluating the ranked possible sites for novel disulfide linkage according to expert rule criterion.

The invention additionally includes a computer apparatus, which comprises a processor means comprising:

(a) first means for selecting a first candidate target amino acid residue of a protein,

(b) second means for selecting a second candidate target amino acid residue of the protein,

(c) means for calculating the error obtained when a known disulfide bond is superimposed on the two candidate target amino acid residues of the protein.

The invention also includes a computer apparatus which comprises a processor means comprising:

(a) first means for selecting a first candidate target amino acid residue of a protein,

(b) second means for selecting a second candidate target amino acid residue of the protein,

(c) means for calculating the error obtained when a known disulfide bond is superimposed on the two candidate target amino acid residues of the protein, and

(d) a display means connected to the processor means, the display means comprising a means for displaying to a user upon command the possible disulfide bond between the cysteine residues, whereby computer-designed protein molecules can be displayed.

The invention also pertains to a computer apparatus, which comprises a processor means comprising:

(a) first means for selecting a first candidate target amino acid residue of a protein,

(b) second means for selecting a second candidate target amino acid residue of the protein,

(c) means for calculating the error obtained when a known disulfide bond is superimposed on the two candidate target amino acid residues of the protein; wherein:

the processor means includes a central processing unit, a storage device, an operating system, and application software; and

the display means includes a visual display monitor, an input device, a storage device, a local processor, and display application software.

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BRIEF DESCRIPTION OF THE FIGURES

The invention may be better understood with reference to the following description read in conjunction with the following figures:

Figure 1 shows in diagrammatical form the five general steps of the computer based method of the invention. The numbers displayed in the Figure represent the following: 1) Preparation of library of known disulfide bonds; 2) Selection of a pair of candidate amino acid residues; 3) Calculation of the distance between the centers-of-mass of the selected candidate residues; 4) Determination of whether calculated distance is within library range; 5) Calculation of extent of fit between atoms of selected residues and disulfide bonds in library; 6) Determination of whether fit is acceptable; 7) Discard selected pair; 8) Record made of fit; 9) Calculation of second best bit; 10) Determination of whether second best fit is acceptable; 11) Record made of second best fit; 12) Discard second best fit; 13) Prepare a list of records; 14) Scan list of recorded fits; 15) Calculation of number and kind of short contacts; 16) Determination of whether number and kind of short contacts are acceptable; 17) Discard potential site; 18) Interactive 3-D graphics display of possible candidate pairs; 19) User initiated ranking of candidate pairs; 20) Expert rule criteria analysis; 21) Identification of potentially protein-stabilizing disulfide bond.

Figure 2 shows a block diagram of computer hardware suitable for use with the computer based method of the invention.

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Figure 3 shows a block diagram of a preferred version of computer hardware suitable for use with the computer based method of the invention.

Figure 4 shows a diagrammatical representation of the algorithm for selecting potential disulfide bond sites of the invention.

Figure 5 shows a representation of a computer program displaying the steps of the algorithm of the computer based method of the invention.

Figure 6 shows a representation of the "Locate Standard Pyramid at Amino Acid X" procedure of the computer based method of the invention.

Figure 7 shows a representation of the "Calculate Distance Between Pyramids" procedure of the computer based method of the invention.

Figure 8 shows a representation of the "Calculate RMS Error vs. pyr#1:pyr#2" procedure of the computer based method of the invention.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

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I.   BRIEF OVERVIEW OF THE INVENTION

The invention provides a method for identifying possible sites within a protein molecule at which cysteine residues might be introduced to replace the normally present amino acid residues. These cysteine residues would then be permitted to form disulfide bonds with each other. By correctly selecting the sites for cysteine incorporation, these disulfide bonds determined by the invention will add to the stability of the folded active protein conformation. The methods and proteins of the present invention are disclosed in co-pending, commonly assigned United States patent application Serial Number 034,964   , filed concurrently with this application by Pantoliano, M.W., *et al.*, which reference is hereby incorporated by reference.

The present invention provides a method for evaluating a protein's structure to determine whether the protein contains at least two target amino acid residues. An amino acid residue is considered to be a "target" residue if its replacement with a cysteine residue would be sufficient to permit the formation of at least one potentially-stabilizing disulfide bond. As used herein, the terms disulfide bond, disulfide linkage, and disulfide bridge are meant to be interchangeable and equivalent. An amino acid which is being evaluated to determine whether it may serve as a target amino acid residue is termed a "candidate target" amino acid residue. Any amino acid residue of protein may, thus, be considered as a "candidate target" amino acid residue; however, only certain amino acid residues will fulfill the requirements of a "target" residue.

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To accomplish the above-described goals, the present invention employs a computer based method for determining and displaying possible sites within natural or engineered proteins where cysteine residues could be inserted to replace the naturally-occurring amino acid residue so that a disulfide linkage would form when the modified protein was mildly oxidized. If the original protein contains one cysteine suitably related to another amino acid, it may be sufficient to change only one amino acid to produce the novel disulfide linkage. In most cases, however, it will be necessary to introduce two cysteine residues into the engineered protein. The original natural protein is referred to as the "wild-type protein." In contrast, the protein which contains the introduced cysteine residues is referred to as the "engineered protein." The terms "disulfide bridge", "disulfide bond", and "cystine" are meant to be equivalent and to describe the structure formed from the disulfide bonding of two cysteine residues to one another.

A.   Thermodynamic Considerations

Although disulfide bonds possess the capacity for stabilizing the folded state of a protein molecule, the presence of a disulfide bond does not control whether the bond will promote protein folding or unfolding. In order to determine the effect of a disulfide bond on protein structure, it is necessary to consider the effects of that bond on the free energy of the folded protein molecule and the unfolded protein molecule.

The free energy of a molecule is a thermodynamic measure of the conformation of a molecule. To increase

the stability of a protein, one must either lower the
free energy of the folded state, or raise the free
energy of the unfolded state. The free energy of a
molecule is determined from the formula:

$$G = H - T(S)$$

where G represents the free energy of protein unfolding
(folded   unfolded), H represents the change in
enthalpy of reaction, T represents the temperature, and
S represents the change in free entropy. At low
temperature, the value H exceeds the product of
temperature and S. Thus G is a positive value and the
folded state of the protein will predominate.   In
contrast, as the temperature is raised the product of
temperature and free entropy eventually exceeds the
value of H and causes G to become a negative number.
When   G is less than zero, protein unfolding will
predominate. Thus, if one could decrease the value of
S, the folded state would be more stable even at higher
temperatures.   Lowering   S may be accomplished by
providing either more disorder within the folded state,
or by decreasing the disorder of the unfolded state.

The introduction of disulfide bonds may increase
the stability of natural proteins by lowering the
disorder of the unfolded protein state.   Amino acids
that are distant in sequence would normally be free to
be far apart in the unfolded state, but this freedom
would be lost if the residues were linked by a disulfide
bond. For this linkage to actually stabilize the folded
state, the disulfide bond must not adversely affect H
or impose additional order on the folded state. This
means that the disulfide bond must fit into the normal

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protein conformation without straining it. Importantly, the further the two cysteines residues are from one another in the primary protein structure, the greater will be the affect upon the S. Thus, linking two distant cysteine residues should destabilize the unfolded protein state much more than a similar linkage between two closely adjacent cysteine residues.

The invention may be operated on a conventional minicomputer system having storage devices capable of storing the Brookhaven protein data bank or an equivalent data base, various applications programs utilized by the invention, and the parameters of the possible candidates that are being evaluated.

The mini-computer CPU is connected by a suitable bus to an interactive computer graphics display system. Typically, the interactive computer graphics display system comprises a display terminal with resident three-dimensional application software and associated input and output devices, such as X-Y plotters, position control devices (potentiometers, an X-Y tablet, or a mouse), and keyboard.

The interactive computer graphics display system allows an operator to view the chemical structures being evaluated in the design process of the invention. Graphics and programs are used to evaluate the possible conflicts between new disulfide bridges and retained atoms of the wild-type protein.

B.   The Five General Steps of the Computer Based Method

It is initially necessary to select a particular protein molecule whose enhanced stability is desired.

The three-dimensional structure of the protein molecule
is determined by means known in the art. Once this
structure has been ascertained it is possible to employ
the novel method of the present invention. The five
general steps of the computer based method are
diagrammed in Figure 1.

1.   The First General Step

The first general step of the computer based method
of the invention involves the compilation of a library
of acceptable geometries which are defined by disulfide
linkages between regions of protein main chain. Such a
library can be constructed from the Brookhaven Protein
Data Bank (BPDB) (Brookhaven Protein Date Base, Chemis-
try Dept., Brookhaven National Laboratory, Upton, NY
11973) or equivalent data bases.

To produce such a library one ascertains the bond
distances and bond angles associated with all atoms of
the two cysteine residues of disulfide bonds which are
present in proteins whose three-dimensional structure
has previously been elucidated. Each entry of this
library must have acceptable bond distances and bond
angles, and must differ in internal geometry from all
other entries in the library. The construction of this
library need not be repeated unless the library is to be
enlarged.

For each disulfide bond entered into the library,
it is necessary to record the positions of all 14 non-
hydrogen atoms of the disulfide bonds (seven from each
cysteine; main chain N, alpha C, beta C, S, carbonyl C,
carbonyl O, and N of next residue). From these
coordinates, one can calculate the dihedral angle along

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the bond which joins the two sulfur atoms. This angle
is called "CHI$_3$" (CHI$_3$ as used in this application
arbitrarily has the opposite sign from the usual CHI$_3$
defined in the literature, i.e., 244° = 116°). Such
bond angles are referred to as the "characterizing" bond
angles of a disulfide bond.

It has been noted by the inventors that there are
cases in which two or more observed disulfide bridges
can be superimposed to high degree of accuracy
considering the atoms N, alpha C, beta C, and carbonyl C
on each side of the disulfide bridge, but that the S
atoms do not match at all well. In such cases, one
disulfide bridge has CHI$_3$ near 90 degrees while the
other has CHI$_3$ near -90 degrees. When the main-chain
atoms are in such a relationship, the geometry of the
disulfide group is determined by the surrounding atoms.

2. The Second General Step

As can be seen in Figure 1, the second general step
of the computer based method of the invention involves
examining each pair of amino acid residues in the
protein of interest to see if they contain certain atoms
whose relative three-dimensional positions possess the
same geometric conformation as the corresponding atoms
of some known disulfide bridge. This examination is
done automatically by the computer program, which
evaluates the library prepared in the first general step
of the present invention. The atoms checked in this
step are the main-chain nitrogen, the alpha carbon, the
beta carbon, and the carbonyl carbon of the two amino
acids of the selected pair. Within each amino acid,
these four atoms form a pyramid with the alpha carbon at

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the apex and with no easily-changed internal degrees of
freedom.

The computer program which implements the second
general step is broken into two phases. The first phase
examines the distance between the centers-of-mass of the
pyramids formed within each of the two amino acids of
the selected pair. If the distance between the two
centers-of-mass is greater than the largest known
distance of any of the disulfide linkages in the
library, or smaller than the smallest known distance of
any of the disulfide linkages in the library, then the
selected pair of residues is discarded and the next pair
of residues is considered. Alternatively, if the
distance between the centers-of-mass of the two residues
fall within the range of inter-pyramid distances in the
library then the second phase of the second general step
is executed for this pair of residues.

In the second phase of the second general step of
the present invention, the eight atoms forming the
pyramids of the two residues in question are considered
as a single group having eight three-dimensional
coordinates. The structure of this 8-atom group is
compared (according to the method of least squares) to
each of the different disulfide bridges contained in the
library. The root-mean-squared (RMS) error for the fit
of the selected amino acid pair as compared to each
different observed disulfide bond in the library is
recorded in computer memory. If for at least one
observed disulfide bridge, the RMS error falls below a
preset limit then the residue pair in question is
recorded as passing the second general step. This
preset limit may vary between 0.3 - 0.6 A and is
preferably set to a value within the range 0.4 - 0.5 A.

When a residue pair passes the second general step an external record is provided which indicates the amino acid pair in question, the identity of the disulfide bond which possess the similar geometry, the RMS error of the analysis and the value of CHI_3 of the fit. After this information has been recorded, the computer program searches for a second fit with the restriction that the CHI_3 must differ from the CHI_3 of the best fit by some preset amount (preferably between 15 - 25 degrees). If such a second-best fit has a RMS error which is below the threshold written above, then a second record is written indicating the amino acid pair involved, the disulfide bond which provides the second best fit, the RMS error of this second-best fit, and the value of CHI_3 of the second-best fit.

If the RMS error does not fall below the preset limit for any of the recorded disulfide linkages, then the current residue pair is rejected and the next pair is examined. For example, with a particular protein of 141 amino acids (such as for example staphylococcal nuclease), 387 amino acid pairs will pass phase one of the second general step. However, only 27 sites will pass phase two of step two and thus be subject to further consideration. The number of sites to be tested will rise as the square of the number of amino acids which comprise the protein, however, the number of good candidates will rise only linearly with this number. The linear rise in the number of good candidates is a result of the limited number of close neighbors which any residue can have.

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3. The Third General Step

In the third general step of the computer based method, the sites listed in the second general step are examined by a computer program to see if the new atoms of the disulfide linkage can be accommodated without altering the tertiary conformation of the protein molecule. Specifically, the new sulfurs of the disulfide bond (to be incorporated into the protein molecule) are positioned according to the observed disulfide which matched best at the site in question in step two. If either or both of the wild-type amino acids are glycines, beta carbons are added as needed. The distance between the sulfurs (and carbons, if new) and all nearby atoms are calculated and a list of distances shorter than physically reasonable (i.e., a list of possible steric contacts) is recorded. This list is divided into two categories based upon the kind of interaction involved: interactions with main-chain atoms and interactions with side-chain atoms (the beta carbon is included as a main chain atom because it cannot be moved by rotation about the side-chain bonds). To allow for flexibility in the protein and for possible errors in the coordinates recorded in the library, a separation distance at which a contact is taken as unreasonably short is set to some preset amount. This preset amount is smaller than the sum of the van der Waals radii of the atoms in question. This preset value is preferably between 0.4 - 0.6 A, however other values could be used.

Because protein side-chains can rearrange more easily than the main chain, short contacts between atoms of the disulfide bond, and main-chain atoms are

considered as potentially more damaging than contacts
with side-chain atoms. The sites selected in step two
are ordered according to the number of main-chain short
contacts. If several sites have identical numbers of
main-chain short contacts, these sites are ordered
according to the number of side-chain short contacts.

In one embodiment, all sites selected in general
step two are passed through to step four with a notation
of how many sterically unacceptable contacts exist in
each category. An expert user reviews this list and
excludes sites with excessive numbers of such contacts.

4.   The Fourth General Step

In the fourth general step of the computer based
method, an expert operator uses an interactive three-
dimensional computer graphics display to view each of
the disulfide bond candidates and to rank them from
those most likely to stabilize an engineered protein
(relative to the wild-type protein), to those least
likely to stabilize the protein. This ranking is done
by considering:

1. the number of short contacts recorded in
   general step three,

2. whether any of these short contacts can be
   relieved by slight changes in side-chain or
   main-chain conformation, or

3. the length of the polypeptide loop created by
   the disulfide bridge.

5. The Fifth General Step

In the fifth general step of the present invention, sequences of proteins evolutionally related to the wild-type protein are used to discover which amino acids may be most easily altered without seriously reducing the stability of the protein. If many sequences are available for similar proteins from a variety of sources, it may be observed that certain residues are strongly conserved in evolution. This conservation will indicate that, in a given location, one particular amino acid is strongly preferred to give an active, stable protein. At many other locations, however, a plurality of amino acids may be acceptable. This information is used to further rank the candidates to determine which of the possible pairs of residues are most likely to give a stabilizing disulfide bridge. If all other factors are equal, those sites which involve no conserved amino acids are much more likely to give a stabilized disulfide bridge than a site which involves one conserved amino acid, which in turn is much more likely to give a stabilizing disulfide bridge than a site which involves two conserved amino acids.

The elected candidates provide potential sites at which pairs of cysteine residues may be introduced. Mild oxidation of the resulting engineered proteins will give rise to proteins containing disulfide bridges. The method of selecting the sites described in general steps 1-5 makes it highly likely that the resulting engineered proteins will have the same tertiary structure and biological activity as the initial wild-type protein. Moreover, it is highly likely that the engineered proteins will be more stable with regard to agents which

cause proteins to unfold (i.e., elevated temperature, altered pH, organic solvents, detergents, or chaotropic salts).

The parameters of the candidates can be stored for later use. They can also be provided by the user either visually or recorded on a suitable medium (paper, magnetic tape, color slides, CRT, etc). The results of the various steps utilized in the analysis can be stored for later use or examination. The present invention can be programmed so that certain expert rules are utilized to eliminate unsuitable candidates before they are presented to the operator. These expert rules can be modified based on experimental data as more proteins are modified by introduction of disulfide bridges, or as more natural proteins containing disulfide bridges are added to the data base used in general step one.

II.   The Invention in Detail

A.   The Hardware and Software Environment

A block diagram of the hardware aspects of the computer based method is found in Fig. 2. A central processing unit (CPU) 102 is connected to a first bus (designated massbus 104) and to a second bus (designated Unibus 106). A suitable form for CPU 102 is a model Vax 11/780 made by Digital Equipment Corporation of Maynard, Massachusetts. Any suitable type of CPU, however, can be used.

Bus 104 connects CPU 102 to a plurality of storage devices. In the best mode, these storage devices include a tape drive unit 106. The tape drive unit 106 can be used, for example, to load into the system the

data base of the amino acid sequences whose three
dimensional structures are known. A suitable form for
tape drive 106 is a Digital Equipment Corporation model
TU 78 drive, which operates at 125 inches per second,
and has a 1600-6250 bit per inch (BPI) dual capability.
Any suitable type of tape drive can be used, however.

Another storage device is a pair of hard disk units
labeled generally by reference numeral 108. A suitable
form for disk drive 108 comprises two Digital Equipment
Corporation RM05 disk drives having, for example, 256
Mbytes of storage per disk. Another disk drive system
is also provided in the serial processor mode and is
labeled by reference numeral 110. This disk drive
system is also connected to CPU 102 by bus 104. A
suitable form for the disk system 110 comprises three
Digital Equipment Corporation model Ra 81 hard disk
drives having, for example, 450 Mbytes of storage per
disk.

Dynamic random access memory is also provided by a
memory stage 112 also connected to CPU 102 by bus 104.
Any suitable type of dynamic memory storage device can
be used. In the serial processor mode, the memory is
made up of a plurality of semi-conductor storage devices
found in a DEC model ECC memory unit. Any suitable type
of dynamic memory can be employed.

The disk drives 108 and 110 store several different
blocks of information. For example, they store the data
base
containing the amino acid sequences and structures that
are read in by the tape drive 106. They also store the
application software package required to search the data
base in accordance with the procedures of the present
invention. They also store the documentation and

executables of the software. The hypothetical molecules
that are produced and structurally examined by the
present invention are represented in the same format
used to represent the protein structures in the data
base. Using this format, these hypothetical molecules
are also stored by the disk drives 108 and 110 for use
during the structural design process and for subsequent
use after the process has been completed.

A Digital Equipment Corporation VAX/VMS (DEC
Trademark) operating system allows for multiple users
and assures file system integrity. It provides virtual
memory, which relieves the programmer of having to worry
about the amount of memory that is used. Initial
software was developed under versions 3.0 to 3.2 of the
VAX/VMS operating system. The current embodiment
presently is running on version 4.4. DEC editors and
FORTRAN compiler were utilized.

The CPU 102 is connected by bus 106 to a
multiplexer 114. The multiplexer allows a plurality of
devices to be connected to the CPU 102 via bus 106. A
suitable form for multiplexer 114 is a Digital Equipment
Corporation model Dz 16 terminal multiplexer. In the
preferred embodiment, two of these multiplexers are
used. The multiplexer 114 supports terminals (not shown
in Figure 2) and the serial communications (at 19.2
Kbaud, for example) to the computer-graphics display
system indicated by the dash lined box 116.

The computer-graphics display system 116 includes
an electronics stage 118. The electronic stage 118 is
used for receiving the visual image prepared by CPU 102
and for displaying it to the user on a display
(typically one involving color) 120. The electronic
stage 118 in connection with the associated subsystems

of the computer-graphics display system 116 provide for
local control of specific functions, as described below.
A suitable form of the electronics system 118 is a model
PS 320 made by Evans & Sutherland Corp. of Salt Lake
City, Utah.   A suitable form for the display 120 is
either a 25-inch color monitor or a 19-inch color
monitor from Evans & Sutherland.

     Dynamic random access memory 122 is connected to
the electronic stage 118.   Memory 122 allows the
electronic system 118 to provide the local control of
the image discussed below.   In addition, keyboard 124 of
conventional design is connected to the electronic stage
118, as is an x/y tablet 126 and a plurality of dials
128. The keyboard 124, x/y tablet 126, and dials 128 in
the serial processor mode are also obtained from Evans &
Sutherland.

     The computer generated graphics system 116, as
discussed above, receives from CPU 102 the image to be
displayed. It provides local control over the displayed
image so that specific desired user initiated functions
can be performed, such as:

          (1)   zoom capacity (so as to increase or decrease
                the size of the image being displayed);

          (2)   clipping capacity (where the sides, front or
                back of the image being displayed are
                removed);

          (3)   intensity depth queuing (where objects further
                away from the viewer are made dimmer so as to
                provide a desired depth effect in the image
                being displayed);

          (4)   translation capacity (allowing translation of
                the image in any of the three axes of the

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coordinate system utilized to plot the molecules being displayed);

(5)   rotation capacity (allowing rotation in any of the three directions of the image being displayed);

(6)   on/off control of the logical segments of the picture. For example, a line connecting the alpha carbons of the protein might be one logical segment; labels on some or all of the residues of the protein might be a second logical segment; a trace of the disulfide candidate might be a third segment; and a stick figure connecting Carbon, Nitrogen, Oxygen, and Sulphur atoms of the adjacent residues of the protein might be a fourth logical segment. The user seldom wants to see all of these at once; rather the operator first becomes oriented by viewing the first two segments at low magnification. Then the labels are switched off and the disulfide trace is turned on. Once the general features of the disulfide candidate are seen, the operator zooms to higher magnification and turns on the segments which hold more detail;

(7)   selection of atoms in the most detailed logical segment. Despite the power of modern graphics, the operator can be overwhelmed by too much detail at once. Thus the operator will pick one atom and ask to see all amino acids within some radius of that atom, typically six Angstroms, but other radii can be used. The user may also specify that certain amino acids will be included in

addition to those that fall within the specified radius of the selected atom;

(8) changing of the colors of a various portion of the image being displayed so as to indicate to the viewer particular information using visual queuing.

As stated above, in the preferred embodiment of the present invention the application software is run on version 4.4 of the Vax/Vms operating system used in conjunction with CPU 102. The application programs were programmed using the FLECS (FORTRAN Language with Extended Control Sections) programming language written in 1974 by Terry Beyer of the University of Oregon, Eugene, Oregon. The FLECS is a FORTRAN preprocessor, which allows more logical programming. All of the code used in the current embodiment was developed in FLECS. It can be appreciated, however, that the present invention encompasses other operating systems and programming languages.

The macromolecules displayed on color display 120 of the computer-graphics display system 116 utilize an extensively modified version of version 5.6 of FRODO. FRODO is a program for displaying and manipulating macromolecules. FRODO was written by T.A. Jones at Max Planck Institute for Biochemistry, Munich, West Germany, for building or modeling in protein crystallography. FRODO version 5.6 was modified so as to be driven by command files; programs were then written to create the command files. It is utilized by the electronic stage 118 to display and manipulate images on the color display 120. Again, any suitable type of program can be used for displaying and manipulating the

macromolecules, the coordinates of which are provided to the computer-graphics display system 116 by the CPU 102.

Design documentation and memos were written using PDL (Program Design Language) from Caine, Farber & Gordon of Pasadena, California. Again, any suitable type of program can be used for the design documents and memos.

Fig. 3 shows in block diagram form a preferred version of the hardware system of the present invention. Like numbers refer to like items of Fig. 2. Only the differences between the serial processor mode system of Fig. 2 and the improved system of Fig. 3 are discussed below.

The CPU 102' is the latest version of the Vax 11/780 from Digital Equipment Corporation. The latest processor from DEC in the VAX product family is approximately ten times faster than the version shown in the serial processor mode of Fig. 2.

Instead of the two Rm05 disk drives 108 of Fig. 2, the embodiment of Fig. 3 utilizes five RA 81 disk drive units 110'. This is to upgrade the present system to more state of the art disk drive units, which provide greater storage capability and faster access.

Serial processor 106 is connected directly to the electronic stage 118' of the computer-graphics display system 116. The parallel interface in the embodiment of Fig. 3 replaces the serial interface approach of the serial processor mode of Fig. 2. This allows for faster interaction between CPU 102' and electronic stage 118' so as to provide faster data display to the expert operator.

Disposed in front of color display 120 is a stereo viewer 202. A suitable form for stereo viewer 202 is

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made by Terabit, Salt Lake City, Utah. Stereo viewer
202 would provide better 3-D perception to the expert
operator than can be obtained presently through rotation
of the molecule.

In addition, this embodiment replaces the FRODO
macromolecule display programs with a program designed
to show a series of related hypothetical molecules.
This newer program performs the operations more quickly
so that the related hypothetical molecules can be
presented to the expert operator in a short enough time
that makes examination less burdensome on the operator.

The program can be modified so as to cause the
present invention to eliminate candidates in the third
general step where the new disulfide bridge would
obviously crowd retained atoms of the wild-type protein.

In addition, the third general step can be refined
in several ways. For example, the model volumes of the
atoms in the neighborhood of the new disulfide bridge
could be calculated. Here the volume of an atom means
the volume of space closer to that atom than to any
other. Thus an atom in a loosely-packed region will
appear to have a large volume. Atoms with large volumes
can move more easily than atoms with small volumes.
Thus a short contact between a new atom and a retained
atom which has large volume is less damaging than a
short contact with a retained atom of small volume.
Using standard energy-minimization programs, one can
eliminate most bond stretching, bond bending, bond
torsion, and unfavorable non-bonded interactions.
Calculation of the volumes of all atoms in the region
will show whether a suitable geometry has been obtained.
A geometric distribution of atoms in which each atom has
the same volume as other atoms of the same type in

natural proteins is more likely to correspond to a
stabilized protein than one in which the atomic volumes
depart widely from observed averages.

Another method which could be used to estimate the
probable stabilizing influence of new disulfide bridges
is molecular dynamics. Molecular dynamics could be
used to determine whether atoms in the neighborhood of
the new disulfide bridge can rearrange to accommodate
the new crosslink.

B.   The Preparation of the Library of Disulfide
       Linkages

The Brookhaven Protein Data Bank (BPDB) contains
structures for between 250 and 300 proteins. Many of
these structures contain disulfide bridges. Because
this collection of structures has been obtained from
many different laboratories over several years, there is
substantial variation in the quality of structures.
Most protein structures are refined against diffraction
data subject to constraints or restraints. Many
proteins do not diffract x-rays very well and
consequently insufficient data exists to determine the
position of each atom. Furthermore, until quite
recently collection of protein diffraction data was
very laborious so that crystallographers often did not
collect all the data that could be collected.

Crystallographers generally assume that all bond
distances and angles are the same as or very close to
the distances and angles determined in small-molecule
structures where every atom can be localized very
accurately. These added data make it possible to
construct models of proteins in which each non-hydrogen

atom is represented by an x-y-z triplet plus an
isotropic temperature factor.

As the methods of the present invention utilize the
geometric relationship between two amino acids which
might be connected by a disulfide bridge, the most
important point to determine about each reported
disulfide bridge is whether the report is correct. The
eight main-chain atoms have 24 degrees of freedom.
Least-squares fitting of a standard pyramid (containing
the nitrogen, carbonyl carbon, alpha carbon, and beta
carbon of an amino acid) at each end filters out most of
the noise in the report coordinates. Finally the six
degrees of freedom relating the two standard pyramids
are calculated. The November 1986 release of BPDB
contained 512 reported disulfide bridges.

Those disulfide linkages which departed from
average distances by more than 10% were considered
suspicious. The data obtained from these structures may
however still be useful, because all that is required is
1) that a disulfide bridge does, in fact, exist, and 2)
the nature of the relationship between the two segments
of main chain. Thus reported disulfide bridges with
incorrect intersulfur distances are not simply rejected,
rather attempts to impose correct internal geometry by
small movements of the sulfur atoms (i.e., less than 0.2
A) or very small movements of the beta carbons (less
than 0.1A) are made.

Once disulfide bonds with unacceptable and
unrepairable geometry are rejected, the program compares
each reported disulfide with all others to eliminate
geometric duplicates. For this purpose, two disulfide
bonds are considered the same if ten of their atoms can
be superimposed on the corresponding atoms with an RMS

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error less than 0.2 A.   Removal of duplicates reduced the original 512 reported disulfide bonds to 138 unique ones.

In order to further refine the three-dimensional configuration and intersulfur distances of the disulfide bridges, the pyramid formed from the nitrogen, alpha carbon, beta carbon and carbonyl carbon of the individual cysteines is examined. These 4 atoms have 12 coordinates, yet only 6 degrees of freedom. The pyramids formed from both of the cysteine residues are evaluated as follows. The 8 atoms (of the two pyramids) are translated until one pyramidal cluster set of 4 atoms has its center of mass at the origin. The constellation of 8 atoms is then rotated so that the plane formed by the nitrogen, carbonyl carbon, and the beta carbon is parallel to the X-Y plane. The alpha carbon is then positioned so as to have a positive Z coordinate (the other 3 atoms of the pyramid thus have the same negative Z coordinate). The pyramid is then rotated about the Z axis until the nitrogen atom has a zero Y coordinate. This defines the standard position for the pyramid. The coordinates of this group are shown in Table 1.

Table 1 Standard N-Ca-Cb-C Pyramid

		X	Y	Z
N	(nitrogen)	+1.40047	+0.00000	-0.11897
Ca	(alpha C)	+0.01174	+0.00259	+0.35693
Cb	(beta C)	-0.70690	+1.25305	-0.11897
C	(carbonyl C)	-0.70531	-1.25564	-0.11897

For each different disulfide bond, an external record is written recording:

1)   the protein in which the disulfide occurs,

2)   the two amino acids involved,

3)   the length of the vector from the center of
      one pyramidal cluster to the other (spherical
      polar coordinate, r),

4)   the spherical polar angular coordinates phi
      and theta of the center of the second cluster,

5)   the three rotations needed to orient the
      second cluster about its center,

6)   the value of <u>CHI</u>$_3$, the S--S dihedral angle.

This list of different observed disulfide bridges
is used each time sites for introduction of disulfide
bonds are sought for a protein which is to be
stabilized.   The library need be updated only when one
obtains new protein structures containing potentially
novel disulfide bridges.

C.   <u>The Selection of Sites to Stabilize a Protein</u>.

     1.   <u>The Process in General</u>

     The process for selecting sites to stabilize a
protein is conducted through the use of a computer. The
algorithm followed by this program is composed of six
different steps. The algorithm is depicted in Figure 4.
First, in the manner described above, a pyramid whose
vertices correspond to the standard coordinates of an
amino acid in the protein under study is prepared. This
amino acid is designated by the letter "K" and initially
(K=1) corresponds to the first amino acid of the protein
molecule.   A similar standard coordinate pyramid is
produced for a second amino acid of the protein under
investigation. This second amino acid is designated by

the letter "L." Initially, amino acid "L" is one amino acid away from amino acid "K" (i.e., initially, L = K + 1). Once the two coordinate pyramids have been prepared, the distance between them is calculated. The computer program then determines whether the calculated distance between the two pyramids is within the bounds of the disulfide linkages stored in the library data base. If the calculated distance is not within the bounds of the library, L is tested against N. If L equals N, then K is tested against N-1. If K is less than N-1, then K is set to K+1 and L is set to 1 and the process iterates. If L was less than N, the L is increased by 1 and the process iterates. If K=N-1 aand L=N, then all pairs have been examined.

If the distance between two calculated pyramids is found to be within the bounds of the values present in the library, then an eight-atom image is constructed from the N, C alpha, C beta, and C carbonyl of each of the two pyramids. The computer program then scans the library of known disulfide linkages to find that linkage with the lower RMS error between the eight atoms of the target protein and the corresponding eight atoms from a library entry. The program then repeats its scan in order to identify a second best fit disulfide linkage, subject to the restriction that CHI_3 for the second-best fit must differ from CHI_3 of the best fit by at least some preset amount, 20° in preferred embodiment. Both the best fit and second best fit are recorded and stored for future use. The computer program then picks a next pair of amino acids by the same method as that used if the distance between pyramids had not been in range.

In the above-described manner the program loops through all possible amino acids K and L. Location of a

standard pyramid at amino acid K or L exploits the
redundancy of the twelve coordinates which determine the
6 degrees of freedom. If either amino acid K or L is
badly distorted, the computer program advises the user
of this problem and the faulty amino acid is discarded.

As an example, the protein, staphylococcal nuclease
which has 141 amino acids, contains 10,011 amino acid
pairs. Of these, 387 were close enough to define a
distance which was in the bounds of the disulfide
linkages contained in the library.

Significantly, the pair of amino acids being
evaluated is tested in both the direction L to K and the
direction K to L. This is necessary because the
geometries of cystines do not have a two-fold rotational
symmetry about the midpoint of the S--S bond.

Once the RMS errors of the amino acid pair is
determined relative to each disulfide bridge in the
library, the list of RMS errors is scanned to find that
entry which produced the smallest error. If this
smallest error is below the preset threshold (for
example, 0.40 - 0.55 A, and preferably 0.45 A), an
external record is written. The list of RMS errors is
then searched for a second best fit subject to the
condition that the dihedral angle CHI_3 of the second-
best fit must differ from the angle CHI_3 by at least
some minimal preset amount (i.e., 15 - 25 degrees).
This second-best fit is recorded if its RMS error falls
below the preset threshold value.

2. The Process in Detail

The process through which the novel computer
program of the present invention identifies potential

sites for disulfide bond crosslinking may be more fully
explained through reference to Figure 5.

Referring to Figure 5, the DO-loops defined in
lines 6000 and 6030 step through all possible pairs of
amino acids K and L. Location of a standard N-Ca-Cb-C
pyramid at amino acids K and L in lines 6010 and 6040
exploits the redundancy of the twelve coordinates which
determine six degrees of freedom; this process is
explained in further detail in Fig. 6 and in text below.
If either amino acid K or L is badly distorted, the
user is advised of the problem, but no further action is
taken with the faulty amino acid (lines 6020 and 6050).
At line 6060 the program calculates the distance
between the two pyramids, as described in Fig. 7 and in
the text below. The loop from line 6070 to line 6190 is
entered only if the two pyramids are close enough
together that a suitable fit is possible. In examining
the protein staphylococcal nuclease which has 141 amino
acids, 10,011 amino acid pairs were examined. Of these,
387 were close enough that the loop from 6070 to 6190
was entered. At line 6080 a loop over the different
observed disulfide bridges is initiated. At line 6090
the current pair of amino acids is tested with amino
acid K as the first and L as the second. At line 6100
the current pair is tested with L as the first and K as
the second. This is necessary because the geometries of
disulfide linkages do not have two-fold rotational
symmetry about the midpoint of the S--S bond. The
DO-loop begun on line 6080 ends on line 6110. On line
6120 the list of 2*(Number-of-different-observed-
Cystines) RMS-errors is scanned to find the smallest
error. If this smallest error is below the preset
threshold (0.45 A in preferred embodiment), an external

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record is written (line 6140). In line 6150, the list
of RMS errors is searched for a second best fit subject
to the condition that the dihedral angle CHI$_3$ of the
second-best fit must differ from the dihedral angle CHI$_3$
of the best fit by at least some preset amount (20
degrees in preferred embodiment). In lines 6160 through
6180 this second-best fit leads to an external record if
its RMS error falls below the preset threshold.   The
remainder of the procedure closes the various logical
blocks.

      T   h   e   p   r   o   c   e   d   u   r   e
LOCATE_STANDARD_PYRAMID_AT_AMINO_ACID_x is described in
Fig. 6.   In lines 7010 through 7030 glycines in the
wild-type protein are augmented with a fictive beta
carbon which can easily be defined from the locations of
N, Ca, and C.   In lines 7040 through 7044 the procedure
tests to see that all four atoms (N, Ca, Cb, and C) are
present in the model.   If atoms are absent, then lines
7050 through 7080 are not executed and the amino acid x
=(either K or L) is eliminated from further
consideration.   If all atoms are present, then lines
7050 through 7080 are executed.   In line 7060 the
standard N-Ca-Cb-C pyramid is least-squares fit to the
four atoms of the current amino acid x. This means that
the coordinates of the standard pyramid can be
translated or rotated as a group to minimize the
distances between corresponding atoms.   This was
achieved with a public-domain set of subroutines called
MOLFIT written by Dr. James Remington. MOLFIT returns
the RMS_error; in line 7070 the RMS_error is compared to
a preset threshold, 0.2 A in preferred embodiment.
Lines 7080 and 7090 indicate closure of logical locks.

The procedure CALCULATE_DISTANCE_BETWEEN_PYRAMIDS is illustrated in Fig. 7. In line 8010 the coordinates of all four atoms in the K pyramid are summed and the sum divided by 4 to give a center-of-mass for the K pyramid. In line 8020 the center-of-mass of pyramid L is calculated. In line 8030 the separation is calculated as the standard Euclidian distance.

The procedure CALCULATE_RMS_ERROR_VS_pyr#1:pyr#2 is illustrated in Fig. 8. In line 9010, the four atoms from pyramid #1 (K or L) are made to correspond to the four atoms (nitrogen, alpha carbon, beta carbon and carbonyl carbon) of one half-cystine in the disulfide bridge. In line 9020, the four atoms from pyramid #2 (L or K) are made to correspond to the four atoms of the other half-cystine in the observed disulfide bridge. In line 9030 these two collections of eight atoms are rotated and translated as rigid bodies to obtain least squared error between corresponding atoms. The least-squared error is reported in line 9040.

D.   The Elimination of Potential Candidates

The above-described computer program provides a list of potential disulfide linkages which may be used to connect two regions of a protein molecule in an effort to stabilize that molecule. If the group of potential linkages is small, it may be feasible for one to construct protein molecules which possess each of the identified disulfide bridges. If, however, the selected group of linkages is large, it may not be possible to produce an entire set of engineered protein molecules. In such a situation, it is desirable to rank the identified disulfide bridges and to eliminate candidates

which are less likely to provide a stabilizing influence
on the protein of interest.

    1.   Elimination of Candidates Based Upon
          Considerations of Steric Interactions

    The stable folding of proteins is dominated by the
packing of hydrophobic groups against each other and
away from the generally aqueous solvent. It is
essential that the volume inside the protein be nearly
filled and that polar or charged groups make appropriate
interactions with each other or with the solvent
molecules. In natural proteins, some water molecules
are found inside the protein and form hydrogen bonds
with oxygen or nitrogen atoms of the internal surface of
the protein. Many carbon and sulfur atoms (and the
hydrogen atoms covalently bound to these atoms) are
found to be in van der Waals contact with other non-
polar atoms. Proteins form such densely packed
structures because a tightly compressed protein
structure allows greater volume to the water and thus
increases the entropy of the solvent. Hence, protein
structure is not predominantly the result of the very
weak attractive van der Waals forces between the
protein atoms. In natural proteins, atoms are never
closer than their van der Waals radii contact because of
repulsive forces.

    The simplest selection process for potential
disulfide bridges would be to place all the atoms in the
candidate structures and to then calculate the
interatomic separations between the atoms of the
disulfide bridge and all the retained atoms of the
native protein. Candidates in which two atoms appear to

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be closer than permitted would be rejected. This very
simple method is not used for two reasons:

(1)   The recorded protein coordinates may contain
      errors.

(2)   Protein structures are not static, and hence
      some steric hindrance may be permissible.

Thus, in order to eliminate less probable
candidates on the basis of packing considerations, a
more sophisticated analysis is required. A potential
steric interference between the atoms is recorded only
when the atoms are closer than their van der Waals radii
by some preset amount (i.e., preferably 0.4 - 0.6 A).
Moreover, such contacts are divided into two classes
which are separately evaluated. The first considered
class are those in which the potentially interfering
atoms are members of the main-chain of the protein.
Contacts with main-chain atoms are more serious because
the motion needed to relieve any steric interference
might seriously disrupt the tertiary structure of the
protein. In contrast, conflicts between hypothetical
disulfide bridge atoms and atoms in other side chains
might be easily relieved through rotations about side-
chain bonds. Because of these considerations, the beta
carbon is considered a main-chain atom because it is not
moved by rotations about any side-chain bond.

Given the number of sites at which main-chain
groups are correctly related for introduction of a new
disulfide bridge, it is usually possible to find several
of these sites for which there are no short contacts
(i.e., steric interference) with either main-chain atoms
or side-chain atoms.

A second consideration in evaluating possible
disulfide bridges is to not lose favorable hydrophobic

interactions. Thus, conversion of tryptophan, tyrosine, and phenylalanine residues to cysteine is probably unfavorable because this would create a large hole inside the protein. In contrast, conversion of leucine, isoleucine, or methionine into cysteine is only mildly unfavorable.

    2.   <u>Elimination of Candidates Based Upon Considerations of Sequence Conservation</u>

A tenet of evolution is that the replication of genes is not error-free. Each error in copying a gene potentially alters the meaning of the encoded message. Because the genetic code has redundancies, many copying errors are silent and do not result in a change in the amino acid sequence encoded by the gene. For example, a mutation which changes a codon sequence of AAG into the codon sequence AAA would not effect the amino acid sequence of the encoded protein (which would in both cases be the amino acid lysine).

If a particular protein is produced in several different species, then, by comparing their amino acid sequences, it is possible to obtain insight into which amino acid residues appear to have been conserved (and thus probably essential) throughout evolutionary time. In evaluating potential positions for disulfide bridges, it is, therefore, desirable not to remove or alter any evolutionally conserved amino acid sequences. Thus, the number of potential candidate linkages may be reduced through a consideration of evolutionary protein change.

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E.   Recombinant DNA Manipulations

The primary amino acid sequence of a protein is
stored within the deoxyribonucleic acid (DNA) of a cell
capable of producing that protein. Thus, by altering
the DNA which encodes a particular protein, it is
possible to change that protein's primary sequence.
Thus, although it is possible to change a protein's
amino acid sequence either directly (as by
incorporating additional cysteine residues by synthetic
or semi-synthetic methods) or indirectly (as by altering
the DNA or RNA sequence which encodes that protein), it
is far more advantageous to alter the protein's amino
acid sequence indirectly. Indirect means are preferred
because (1) it is far easier to alter DNA or RNA
sequence than to alter protein sequence, and (2) the
capacity of DNA to self replicate enables one to produce
an inexhaustible supply of the desired protein molecule.

The genetic sequences which are capable of
expressing the engineered proteins of the present
invention are advantageously incorporated into self-
replicating DNA plasmids. A plasmid is a covalently
closed circular extrachromosomal DNA molecule. In
general, a plasmid contains two elements: (1) An origin
of replication sufficient to permit the propagation of
the plasmid in a host cell; and (2) a selectable marker
sequence, preferably a gene whose expression confers an
antibiotic resistance to the host cell, sufficient to
enable the maintenance of the plasmid within the host
cell and to facilitate the manipulation of the plasmid
into new host cells.

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In summary, it is preferable to produce the engineered proteins of the present invention by manipulating the DNA sequences which encode those proteins. The manipulated DNA is then preferably incorporated into a plasmid molecule and introduced into a host cell which is capable of expressing such sequences, thereby producing the engineered protein molecule.

As an example, if a wild-type protein contained the amino acid sequence lysine-serine-leucine, then the corresponding DNA sequence might be AAA-TCT-CTT. If one desired to replace the serine with a cysteine residue, one would produce a DNA sequence such as AAA-TGT-CTT. The introduction of this oligonucleotide into the gene which encodes the wild-type protein can be accomplished using the technique of oligonucleotide-directed _in vitro_ mutagenesis (Kunkel, (_Proc. Natl. Acad. Sci. U.S.A._, _82_:488-492 (1985)), Nisbet, I.T., _et al_. (_Gene Anal. Tech._, _2_:23-29 (1985)), and Hines, J.C., _et al._, (_Gene_, _11_:207-218 (1980)), which are incorporated herein by reference). Hence, this method would result in the production of an altered gene which expressed a protein containing a cysteine residue in place of the original serine residue. In a similar manner, a cysteine residue can be incorporated into any position of any protein molecule.

Having now generally described this invention, the same will be better understood by reference to certain specific examples which are included herein for purposes of illustration only and are not intended to be limiting of the invention, unless specified.

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EXAMPLE I

Production of Stabilized Serine Proteases

Serine proteases are proteolytic enzymes which have a serine residue at their active site. Many species of bacteria are known to secrete such serine proteases into the culture medium. Serine proteases can be inhibited by phenylmethanesulfonylfluoride and/or disopropylfluorophosphate. Subtilisin is a serine protease produced by Gram positive bacteria and fungi. The amino acid sequences of seven different subtilisins are known. These include five subtilisins (SBT) from Gram positive bacteria of the genus, _Bacillus_. The subtilisin produced by _Bacillus amyloliquifaciens_ (hereinafter referred to as SBT BPN') was selected as a model protein and used to prepare an engineered, more stable protein. The wild type SBT BPN' enzyme is discussed by Vasantha, _et al._ (_J. Bacteriol._, _159_:811-819 (1984). The three-dimensional structure of SBT BPN' has been determined to a resolution of 1.3 A.

The number of potential pairs of disulfide linkage sites in a protein such as SBT BPN' is obtained from the following equation:

$$\text{Number of possible pairs} = \frac{N\,(N-1)}{2}$$

Hence, for a protein such as subtilisin, which has 275 amino acid residues (i.e., N = 275) 37,675 different pair wise combinations are possible. Without the above-

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described computer method, it would be necessary to evaluate all of these possibilities experimentally.

Therefore, the above-described method for identifying potential sites which could be linked together with disulfide bonds was used in order to predict those linkages which would result in a more stable subtilisin protein. Before the computer method was applied, sites which included any of the residues Ser 221, Ser 125, His 64 or Asp 32 were discarded, since these residues are essential for subtilisin's catalytic activity. The results of the computer search for potential disulfide bond positions is shown in Table 2.

Table 2 Sites Selected for New Disulfide Bridges
Using Geometry and Packing Based on the
1.3 A Crystal Structure of SBT BPN'

Residues linked	Strain GX	RMS[a] error	Short M/C	Short S/C	CHI$_3$
G 7:P201		0.26	1	2	259
Y 21:S236		0.45	0	0	274
T 22:S 87	7159	0.39	0	0	244
G 23:A 88		0.44	4	0	270
V 26:A232		0.45	0	1	259
V 26:L235	7157	0.42	0	0	275
A 29:A114		0.36	0	2	273
A 29:M119		0.44	0	0	149
I 31:G110		0.17	1	2	268
I 35:A 69		0.28	3	0	84
I 35:A 69		0.38	6	0	269
D 36:H 39		0.18	-	-	244
D 41:G 80		0.22	-	-	84
D 41:G 80		0.26	-	-	269
G 47:P 57		0.36	3	3	89
M 50:N109	7168	0.30	0	0	275
P 57:K 94		0.35	-	-	71
A 85:A 88		0.40	-	-	244
V 93:G110		0.38	-	-	268
V 95:I107		0.43	-	-	101
V 95:G110		0.42	-	-	88
N123:A228		0.29	-	-	78
V150:A228		0.36	-	-	93
V150:A228		0.45	-	-	226
A153:V165		0.38	1	0	252
E156:T164		0.29	0	1	89
S163:G193		0.44	-	-	65
V165:K170		0.41	0	2	145
V165:S191		0.23	3	0	101
Y167:K170		0.44	-	-	108
V177:S224		0.44	-	-	226
A179:A223		0.31	-	-	45
A200:H226		0.44	-	-	269
Q206:A216	8307	0.27	0	0	88
A230:V270		0.35	0	1	90
I234:A274		0.41	0	0	274
H238:W241		0.36	0	0	244
T253:A272		0.42	-	-	89
T253:A273	7140	0.29	-	-	93
T253:A273	"	0.29	-	-	226

[a]Only RMS values of 0.45 and below were used in
selecting these candidates.

In Table 2, the residues linked together are denoted using the single letter code for amino acids (see Table 3) and by the amino acid position number. Hence, the first linkage shown (G7:P201) denotes a potential linkage between cysteines which would replace the glycine which appears at position 7 of subtilisin and the proline which appears at position 201. The second column of Table 2 indicates whether a bacterial strain was constructed which expressed a protein having the indicated disulfide linkage. The third column is the RMS error for the best fit of the geometry of the candidate amino acid pair with that of any observed disulfide bond in the Brookhaven Protein Data Bank. The next two columns list the short contacts that occur between main or side-chain atoms (Short M/C; Short S/C) and thus provide an indication of the number of potential points of steric hindrance which are predicted to be present in the engineered protein. The final column of Table 2 provides the CHI_3 angle of the bond in degrees.

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Table 3   Letter Codes for the Naturally
            Occurring Amino Acids

Alanine	ALA	A
Arginine	ARG	R
Aspartic acid	ASP	D
Asparagine	ASN	N
Cysteine	CYS	C
Glutamic acid	GLU	E
Glutamine	GLN	Q
Glycine	GLY	G
Histidine	HIS	H
Isoleucine	ILE	I
Lysine	LYS	K
Leucine	LEU	L
Methionine	MET	M
Phenylalanine	PHE	F
Proline	PRO	P
Serine	SER	S
Threonine	THR	T
Tryptophan	TRP	W
Tyrosine	TYR	Y
Valine	VAL	V

EXAMPLE II

Elimination of Selected Candidates on the Basis
of Packing and Sequence Conservation

Since the subtilisins from several Bacillus strains
have been purified and sequenced, it is possible to
compare these sequences and thereby identify conserved
amino acid residues. In performing this comparison, the
following references were employed:
SBT BPN' (Vasantha et al., J. Bacteriol.
159:811-819(1984)); SBT Carlsberg (Jacobs et al.,
Nucleic Acid Res. 13:8913-8926 (1985)); SBT DY (Nedov et
al., Biol. Chem. 366:421-430 (1985)); SBT
amylosacchariticus (Kurihara et al., J. Biol. Chem.

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247:5619-5631 (1972)); and Mesenticopeptidase (Svendsen
et al., FEBS Lett. 196:228-232 (1986)).

The amino acid sequence of the subtilisin
thermitase from Thermoactinomyces vulgaris is also known
(Meloun et al., FEBS Lett. 183:195-200 (1985)). The
amino acid sequences from two fungal serine proteases
are also partially known: proteinase K (Jany et al.,
Biol. Chem. Hoppe-Seyler 366:485-492 (1985)) and
thermomycolase (Gaucher et al., Methods Enzymol.
45:415-433 (1976)).

These enzymes have been shown to be related to
subtilisin BPN', not only through their primary sequence
and enzymological properties, but also by comparison of
x-ray crystallographic data (McPhalen et al., FEBS Lett.
188:55-58 (1985) and Pahler et al., EMBO J. 3:1311-1314
(1984)). A comparison of subtilisin amino acid
sequences is shown in Table 4.

Table 4 Subtilisin Sequences

Key: 1 Subtilisin BPN'
      2 Subtilisin Amylosacchariticus
      3 Mesenticopeptidase
      4 Subtilisin Carlsberg
      5 Subtilisin DY
      6 Thermitase

Sequences 1-5 are from bacilli.

XXX Conserved in all sequences - (capitalized and
underlined)
XXX Conserved in Bacillus - (capitalized)
xxx Varies within Bacillus - (lower case)

PROTEASE RESIDUE	1	2	3	4	5	6
-7	---	---	---	---	---	TYR
-6	---	---	---	---	---	THR
-5	---	---	---	---	---	PRO

-4	---	---	---	---	---	ASN
-3	---	---	---	---	---	ASP
-2	---	---	---	---	---	PRO
-1	---	---	---	---	---	TYR
1	ALA	ALA	ALA	ALA	ALA	PHE
2	GLN	GLN	GLN	GLN	GLN	SER
3	ser	ser	ser	thr	thr	ser
4	VAL	VAL	VAL	VAL	VAL	ARG
5	PRO	PRO	PRO	PRO	PRO	GLN
6	TYR	TYR	TYR	TYR	TYR	TRP
7	GLY	GLY	GLY	GLY	GLY	GLY
8	val	ile	ile	ile	ile	pro
9	ser	ser	ser	pro	pro	gln
10	gln	gln	gln	leu	leu	lys
11	ILE	ILE	ILE	ILE	ILE	ILE
12	LYS	LYS	LYS	LYS	LYS	GLN
13	ALA	ALA	ALA	ALA	ALA	ALA
14	pro	pro	pro	asp	asp	pro
15	ala	ala	ala	lys	lys	gln
16	leu	leu	leu	val	val	ala
17	his	his	his	gln	gln	trp
18	ser	ser	ser	ala	ala	asp
19	GLN	GLN	GLN	GLN	GLN	ILE
20	GLY	GLY	GLY	GLY	GLY	ALA
21	tyr	tyr	tyr	phe	tyr	glu
22	thr	thr	thr	lys	lys	---
23	GLY	GLY	GLY	GLY	GLY	GLY
24	ser	ser	ser	ala	ala	ser
25	ASN	ASN	ASN	ASN	ASN	GLY
26	VAL	VAL	VAL	VAL	VAL	ALA
27	LYS	LYS	LYS	LYS	LYS	LYS
28	VAL	VAL	VAL	VAL	VAL	ILE
29	ala	ala	ala	ala	gly	ala
30	val	val	val	val	ile	ile
31	ile	ile	ile	leu	ile	val
32	ASP	ASP	ASP	ASP	ASP	ASP
33	ser	ser	ser	thr	thr	thr
34	GLY	GLY	GLY	GLY	GLY	GLY
35	ILE	ILE	ILE	ILE	ILE	VAL
36	asp	asp	asp	gln	ala	gln
37	ser	ser	ser	ala	ala	ser
38	SER	SER	SER	SER	SER	ASN
39	HIS	HIS	HIS	HIS	HIS	HIS
40	pro	pro	pro	pro	thr	pro
41	ASP	ASP	ASP	ASP	ASP	ASP
42	LEU	LEU	LEU	LEU	LEU	LEU
43	lys	asn	asn	asn	lys	ala
44	VAL	VAL	VAL	VAL	VAL	GLY
45	ala	arg	arg	val	val	lys

46	GLY	GLY	GLY	GLY	GLY	VAL
47	GLY	GLY	GLY	GLY	GLY	VAL
48	ALA	ALA	ALA	ALA	ALA	GLY
49	SER	SER	SER	SER	SER	GLY
50	met	phe	phe	phe	phe	trp
51	VAL	VAL	VAL	VAL	VAL	ASP
52	pro	pro	pro	ala	ser	phe
53	ser	ser	ser	gly	gly	val
54	GLU	GLU	GLU	GLU	GLU	GLU
55	thr	thr	thr	ala	ser	gln
56	asn	asn	asn	---	---	asp
57	pro	pro	pro	tyr	tyr	ser
58	phe	tyr	tyr	asn	asn	thr
59	gln	gln	gln	thr	thr	pro
60	ASP	ASP	ASP	ASP	ASP	GLN
61	asn	gly	gly	gly	gly	gly
62	asn	ser	ser	asn	asn	asn
63	ser	ser	ser	gly	gly	gly
64	HIS	HIS	HIS	HIS	HIS	HIS
65	GLY	GLY	GLY	GLY	GLY	GLY
66	THR	THR	THR	THR	THR	THR
67	HIS	HIS	HIS	HIS	HIS	HIS
68	VAL	VAL	VAL	VAL	VAL	CYS
69	ALA	ALA	ALA	ALA	ALA	ALA
70	GLY	GLY	GLY	GLY	GLY	GLY
71	THR	THR	THR	THR	THR	ILE
72	val	ile	ile	val	val	ala
73	ALA	ALA	ALA	ALA	ALA	ALA
74	ALA	ALA	ALA	ALA	ALA	ALA
75	LEU	LEU	LEU	LEU	LEU	VAL
75a	---	---	---	---	---	THR
76	asn	asn	asn	asp	asp	asn
77	ASN	ASN	ASN	ASN	ASN	ASN
78	ser	ser	ser	thr	thr	ser
79	ile	ile	ile	thr	thr	thr
80	GLY	GLY	GLY	GLY	GLY	GLY
81	VAL	VAL	VAL	VAL	VAL	ILE
82	LEU	LEU	LEU	LEU	LEU	ALA
83	GLY	GLY	GLY	GLY	GLY	GLY
84	VAL	VAL	VAL	VAL	VAL	THR
85	ALA	ALA	ALA	ALA	ALA	ALA
86	PRO	PRO	PRO	PRO	PRO	PRO
87	ser	ser	ser	ser	asn	lys
88	ala	ala	ser	val	val	ala
89	ser	ser	ala	ser	ser	ser
90	LEU	LEU	LEU	LEU	LEU	ILE
91	TYR	TYR	TYR	TYR	TYR	LEU
92	ALA	ALA	ALA	ALA	ALA	ALA
93	val	val	val	val	ile	val

94	LYS	LYS	LYS	LYS	LYS	ARG
95	VAL	VAL	VAL	VAL	VAL	VAL
96	LEU	LEU	LEU	LEU	LEU	LEU
97	gly	asp	asp	asn	asn	asp
98	ala	ser	ser	ser	ser	asn
99	asp	thr	thr	ser	ser	ser
100	GLY	GLY	GLY	GLY	GLY	GLY
101	SER	SER	SER	SER	SER	SER
102	GLY	GLY	GLY	GLY	GLY	GLY
103	gln	gln	gln	thr	thr	thr
104	TYR	TYR	TYR	TYR	TYR	TRP
105	SER	SER	SER	SER	SER	THR
106	trp	trp	trp	gly	ala	ala
107	ILE	ILE	ILE	ILE	ILE	VAL
108	ile	ile	ile	val	val	ala
109	asn	asn	asn	ser	ser	asn
110	GLY	GLY	GLY	GLY	GLY	GLY
111	ILE	ILE	ILE	ILE	ILE	ILE
112	GLU	GLU	GLU	GLU	GLU	THR
113	TRP	TRP	TRP	TRP	TRP	TYR
114	ALA	ALA	ALA	ALA	ALA	ALA
115	ile	ile	ile	thr	thr	ala
116	ala	ser	ser	thr	gln	asp
117	ASN	ASN	ASN	ASN	ASN	GLN
118	asn	asn	asn	gly	gly	gly
119	met	met	met	met	leu	ala
120	ASP	ASP	ASP	ASP	ASP	LYS
121	VAL	VAL	VAL	VAL	VAL	VAL
122	ILE	ILE	ILE	ILE	ILE	SER
123	ASN	ASN	ASN	ASN	ASN	LEU
124	MET	MET	MET	MET	MET	LEU
125	SER	SER	SER	SER	SER	SER
126	LEU	LEU	LEU	LEU	LEU	LEU
127	GLY	GLY	GLY	GLY	GLY	GLY
128	GLY	GLY	GLY	GLY	GLY	GLY
129	PRO	PRO	PRO	PRO	PRO	THR
130	ser	ser	thr	ser	ser	val
131	GLY	GLY	GLY	GLY	GLY	GLY
132	SER	SER	SER	SER	SER	ASN
133	ala	thr	thr	thr	thr	ser
134	ALA	ALA	ALA	ALA	ALA	GLY
135	leu	leu	leu	met	leu	leu
136	LYS	LYS	LYS	LYS	LYS	GLN
137	ala	thr	thr	gln	gln	gln
138	ala	val	val	ala	ala	ala
139	VAL	VAL	VAL	VAL	VAL	VAL
140	ASP	ASP	ASP	ASP	ASP	ASN
141	lys	lys	lys	asn	lys	tyr
142	ALA	ALA	ALA	ALA	ALA	ALA

143	val	val	val	tyr	tyr	trp
144	ala	ser	ser	ala	ala	asn
145	ser	ser	ser	arg	ser	lys
146	GLY	GLY	GLY	GLY	GLY	GLY
147	val	ile	ile	val	ile	ser
148	VAL	VAL	VAL	VAL	VAL	VAL
149	VAL	VAL	VAL	VAL	VAL	VAL
150	val	ala	ala	val	val	val
151	ALA	ALA	ALA	ALA	ALA	ALA
152	ALA	ALA	ALA	ALA	ALA	ALA
153	ALA	ALA	ALA	ALA	ALA	ALA
154	GLY	GLY	GLY	GLY	GLY	GLY
155	ASN	ASN	ASN	ASN	ASN	ASN
156	glu	glu	glu	ser	ser	ala
157	GLY	GLY	GLY	GLY	GLY	GLY
158	thr	ser	ser	ser	ser	asn
159	SER	SER	SER	SER	SER	THR
160	GLY	GLY	GLY	GLY	GLY	ALA
161	ser	ser	ser	asn	ser	pro
162	ser	ser	thr	thr	gln	asn
163	ser	ser	ser	asn	asn	---
164	THR	THR	THR	THR	THR	---
165	val	val	val	ile	ile	---
166	GLY	GLY	GLY	GLY	GLY	---
167	TYR	TYR	TYR	TYR	TYR	TYR
168	PRO	PRO	PRO	PRO	PRO	PRO
169	gly	ala	ala	ala	ala	ala
170	LYS	LYS	LYS	LYS	LYS	TYR
171	TYR	TYR	TYR	TYR	TYR	TYR
172	pro	pro	pro	asp	asp	ser
173	SER	SER	SER	SER	SER	ASN
174	val	thr	thr	val	val	ala
175	ILE	ILE	ILE	ILE	ILE	ILE
176	ALA	ALA	ALA	ALA	ALA	ALA
177	VAL	VAL	VAL	VAL	VAL	VAL
178	GLY	GLY	GLY	GLY	GLY	ALA
179	ALA	ALA	ALA	ALA	ALA	SER
180	VAL	VAL	VAL	VAL	VAL	THR
181	asp	asn	asn	asp	asp	asp
182	SER	SER	SER	SER	SER	GLN
183	ser	ser	ala	asn	asn	asn
184	asn	asn	asn	ser	lys	asp
185	gln	gln	gln	asn	asn	asn
186	ARG	ARG	ARG	ARG	ARG	LYS
187	ALA	ALA	ALA	ALA	ALA	SER
188	SER	SER	SER	SER	SER	SER
189	PHE	PHE	PHE	PHE	PHE	PHE
190	SER	SER	SER	SER	SER	SER
191	SER	SER	SER	SER	SER	THR

192	val	ala	ala	val	val	tyr
193	GLY	GLY	GLY	GLY	GLY	GLY
194	pro	ser	ser	ala	ala	ser
195	GLU	GLU	GLU	GLU	GLU	VAL
196	LEU	LEU	LEU	LEU	LEU	VAL
197	asp	asp	asp	glu	glu	asp
198	VAL	VAL	VAL	VAL	VAL	VAL
199	MET	MET	MET	MET	MET	ALA
200	ALA	ALA	ALA	ALA	ALA	ALA
201	PRO	PRO	PRO	PRO	PRO	PRO
202	GLY	GLY	GLY	GLY	GLY	GLY
203	val	val	val	ala	val	ser
204	ser	ser	ser	gly	ser	trp
205	ile	ile	ile	val	val	ile
206	gln	gln	gln	tyr	tyr	tyr
207	SER	SER	SER	SER	SER	SER
208	THR	THR	THR	THR	THR	THR
209	leu	leu	leu	tyr	tyr	tyr
210	PRO	PRO	PRO	PRO	PRO	PRO
211	gly	gly	gly	thr	ser	thr
212	asn	gly	gly	ser	asn	ser
213	lys	thr	thr	thr	thr	thr
214	TYR	TYR	TYR	TYR	TYR	TYR
215	gly	gly	gly	ala	thr	ala
216	ala	ala	ala	thr	ser	ser
217	tyr	tyr	tyr	leu	leu	leu
218	ASN	ASN	ASN	ASN	ASN	SER
219	GLY	GLY	GLY	GLY	GLY	GLY
220	THR	THR	THR	THR	THR	THR
221	SER	SER	SER	SER	SER	SER
222	MET	MET	MET	MET	MET	MET
223	ALA	ALA	ALA	ALA	ALA	ALA
224	ser	thr	thr	ser	ser	thr
225	PRO	PRO	PRO	PRO	PRO	PRO
226	HIS	HIS	HIS	HIS	HIS	HIS
227	VAL	VAL	VAL	VAL	VAL	VAL
228	ALA	ALA	ALA	ALA	ALA	ALA
229	GLY	GLY	GLY	GLY	GLY	GLY
230	ALA	ALA	ALA	ALA	ALA	VAL
231	ALA	ALA	ALA	ALA	ALA	ALA
232	ALA	ALA	ALA	ALA	ALA	GLY
233	LEU	LEU	LEU	LEU	LEU	LEU
234	ILE	ILE	ILE	ILE	ILE	LEU
235	LEU	LEU	LEU	LEU	LEU	ALA
236	SER	SER	SER	SER	SER	SER
237	LYS	LYS	LYS	LYS	LYS	GLN
238	his	his	his	his	tyr	---
239	PRO	PRO	PRO	PRO	PRO	---
240	asn	thr	thr	asn	thr	gly

241	trp	trp	trp	leu	leu	arg
242	thr	thr	thr	ser	ser	ser
243	asn	asn	asn	ala	ala	ala
244	thr	ala	ala	ser	ser	ser
245	GLN	GLN	GLN	GLN	GLN	ASN
246	VAL	VAL	VAL	VAL	VAL	ILE
247	ARG	ARG	ARG	ARG	ARG	ARG
248	ser	asp	asp	asn	asn	ala
249	ser	arg	arg	arg	arg	ala
250	LEU	LEU	LEU	LEU	LEU	ILE
251	glu	glu	glu	ser	ser	glu
252	asn	ser	ser	ser	ser	asn
253	THR	THR	THR	THR	THR	THR
254	thr	ala	ala	ala	ala	ala
255	THR	THR	THR	THR	THR	ASP
256	lys	tyr	tyr	tyr	asn	lys
257	LEU	LEU	LEU	LEU	LEU	ILE
257a	---	---	---	---	---	SER
258	GLY	GLY	GLY	GLY	GLY	GLY
259	asp	asp	ser	ser	asp	thr
260	SER	SER	SER	SER	SER	GLY
261	PHE	PHE	PHE	PHE	PHE	THR
262	TYR	TYR	TYR	TYR	TYR	TYR
263	TYR	TYR	TYR	TYR	TYR	TRP
264	GLY	GLY	GLY	GLY	GLY	ALA
265	LYS	LYS	LYS	LYS	LYS	LYS
266	GLY	GLY	GLY	GLY	GLY	GLY
267	LEU	LEU	LEU	LEU	LEU	ARG
268	ILE	ILE	ILE	ILE	ILE	VAL
269	ASN	ASN	ASN	ASN	ASN	ASN
270	VAL	VAL	VAL	VAL	VAL	ALA
271	gln	gln	gln	glu	glu	tyr
272	ALA	ALA	ALA	ALA	ALA	LYS
273	ALA	ALA	ALA	ALA	ALA	ALA
274	ALA	ALA	ALA	ALA	ALA	VAL
275	GLN	GLN	GLN	GLN	GLN	GLN
276	---	---	---	---	---	TYR

Comparing all sequences, there are 91 completely conserved residues while 194 of the residues vary. The _Bacillus_ sequences are more closely related with 171 of 275 being conserved. The 40 potential disulfide linkage sites identified by the computer program were then analyzed to determine whether any of these linkages would involve the alteration of a conserved amino acid

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residue. Those residue linkages which did not result in
the alteration of a conserved amino acid are shown in
Table 5.

Table 5
Sites Selected for New Disulfide Bridges Using Geometry, Packing, & Homology

Residues linked	Strain GX	RMS[b] error	Short M/C	Short S/C	CHI$_3$
T 22:S 87	7159	0.39	0	0	244
V 26:L235	7157	0.42	0	0	275
G 47:P 57		0.36	3	3	89
M 50:N109	7168	0.30	0	0	275
E156:T164		0.29	0	1	89
V165:K170		0.41	0	2	145
V165:S191		0.23	3	0	101
Q206:A216	8307	0.27	0	0	88
A230:V270		0.35	0	1	90
I234:A274		0.41	0	0	274
H238:W241		0.36	0	0	244

As seen in Table 5, 11 linkages were identified as
possible candidates for introduced disulfide bonds that
would increase the stability of SBT BPN'. The 11
linkages were then examined to identify those linkages
having the least RMS error and the fewest steric
hindrances (short contact main-chain and side-chain
interactions). Six out of these eleven are shown to
have no short contacts with main-chain and side-chain
atoms. Four of these , T22:S87, Y26:L235, M50:N109,
and Q206:A216 were selected for oligonucleotide-directed
mutagenesis, and the variant proteins containing these
selected disulfide bridges were called subtilisin 7159,
7157, 7168, and 8307, respectively.

---

[b]Only RMS values of 0.45 A and below were used in
selecting these candidates.

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EXAMPLE III

Production of Engineered Proteins

Using the technique of oligonucleotide-directed in
vitro mutagenesis, described above, strain GX7157 was
constructed.   In this strain, the SBT BPN' protein
contains cysteine residues at position 26 (replacing
valine) and at position 235 (replacing leucine).   Strain
GX7157 was found to be capable of producing and
secreting subtilisin.   The disulfide bond may have
formed, but the resultant protein was decidedly less
stable than wild-type. It was observed that the single
substitution of a cysteine for the lysine residue at
position 235 was mildly destabilizing. In contrast, the
engineered protein which possessed a cysteine instead of
a valine at position 26 was approximately as stable as
the wild-type protein.

A   second   mutant   strain was   constructed   which
contained   cysteines   at   position   50   (replacing
methionine)   and   position   109   (replacing   asparagine).
This mutant strain was designated GX7168.   Subtilisin
was produced in this strain and secreted, however, the
engineering protein was decidedly less stable than wild-
type.

A third mutant strain was constructed in which the
threonine at position 22 and the serine at position 87
were replaced by cysteines. This mutant was designated
GX7159. ·The subtilisin secreted by this strain was
found to contain the desired disulfide bond.   This
engineered protein was decidedly more stable than wild-
type subtilisin.

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In 10 mM calcium chloride, the rate for thermal inactivation of subtilisin 7159 (i.e., produced from mutant strain GX7159) is 1.1 times slower than wild-type subtilisin BPN' at 65°C. In 1 mM EDTA, the rate of thermal inactivation at 45°C for subtilisin 7159 is 1.5 to 2.0 times slower than that for wild-type subtilisin BPN'. It is well known that subtilisin is stabilized by free calcium ions. Many preparations for washing clothes contain agents to sequester calcium because free calcium interferes with the action of detergents. Thus the improved stability of subtilisin 7159 in a calcium-free environment (i.e., an environment containing EDTA) is especially useful.

In addition, subtilisin 7159 was melted in a differential scanning calorimeter. In 10 mM calcium chloride, subtilisin 7159 melted 0.5°C above the melting temperature of wild-type subtilisin. In 10 mM EDTA, subtilisin 7159 melted 3.1°C above the melting temperature of wild-type subtilisin. Thus, subtilisin 7159 was substantially more thermodynamically stable than the wild-type protein.

A mutant was constructed which contained cysteine residues at position 206 (replacing glutamine) and at position 216 (replacing alanine). This mutant was designated GX8307. The subtilisin secreted by this mutant was found to contain the desired disulfide bond. The subtilisin produced by GX8307 (termed subtilisin 8307) was decidedly more stable than wild-type subtilisin.

In 10 mM calcium chloride, the rate for thermal inactivation at 65°C for subtilisin 8307 is 1.1 times slower than that of wild-type subtilisin BPN'. In 1 mM EDTA, the rate of thermal inactivation at 45°C for

subtilisin 8307 is also 1.5 to 2.0 times slower than
wild-type subtilisin BPN'. In addition, subtilisin 8307
was melted in a differential scanning calorimeter. In
10 mM EDTA, subtilisin 8307 melted about 3.0°C above the
melting temperature of wild-type subtilisin. Thus,
subtilisin 8307 was substantially more stable than the
wild-type protein. Since, as indicated above,
subtilisin is stabilized by free calcium ions, the
improved stability of subtilisin 8307 in a calcium-free
environment is again especially useful for an enzyme to
be introduced into detergents for washing clothes.

Using oligonucleotide-directed mutagenesis, the
disulfide bond of subtilisin 7159 (cysteines at
positions 22 and 87) was combined in the same subtilisin
molecule with a stabilizing mutation (asparagine 218 to
serine) identified by random mutagenesis. (The 218
random mutation is described in co-pending, commonly
assigned PCT Patent Application 87/00348.) This new
subtilisin molecule (subtilisin 7181), which was
secreted by strain GX7181, contained the desired
disulfide bond and was decidedly more stable than wild-
type.

Subtilisin 7181 was crystallized isomorphously to
wild-type subtilisin. Using these crystals, x-ray data
was collected to a resolution of 1.8 A. The phases of
wild-type subtilisin were used to initiate Hendrickson-
Konnert refinement (Hendrickson, W.H. and Konnert, J.H.
(1980) In: Computing in Crystallography, (Diamond, R.,
Ranseshan, S. and Venkatesan, K., eds.), pp. 13.01-
13.23, Indian Institute of Science, Bangalore) which was
continued until the crystallographic R index was 14.5.
The disulfide bridge was found to be in the predicted
conformation.

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In 10 mM calcium chloride, the rate of thermal inactivation of subtilisin 7181 is 4.0 times slower than that of wild-type subtilisin BPN' at 65°C. In 1 mM EDTA, the rate of thermal inactivation at 45°C for subtilisin produced by GX7181 is approximately 5.2 times slower than that of wild-type subtilisin BPN'. In addition, subtilisin 7181 was melted in a differential scanning calorimeter. In 10 mM EDTA, subtilisin 7181 melted 7.5°C above the melting temperature of wild-type subtilisin. Thus, subtilisin 7181 was substantially more stable than the wild-type protein. Thus, the subtilisin produced by GX7181, which exhibits improved stability in a calcium-free environment, is especially useful in preparations which contain detergents.

Also using oligonucleotide-directed mutagenesis, the disulfide bond of subtilisin 7159 (cysteines at positions 22 and 87) was combined with the disulfide bond of subtilisin 8307 (cysteines at positions 206 and 216) to create subtilisin 8310. Subtilisin 8310, produced by strain GX8310, was found to be secreted and to contain both of the desired disulfide bonds. Subtilisin 8310 was melted in a differential scanning calorimeter. In 10 mM EDTA, subtilisin 8310 melted about 5.5°C above the melting temperature of wild-type subtilisin. Thus, subtilisin 8310 was substantially more stable than the wild-type protein.

The reasons for the failure of the disulfide linkages contained in subtilisin 7157 and 7168 to stabilize these proteins is unknown at the present time. Residues Val 26 and Leu 235 which are changed to cysteines in subtilisin 7157 are less variable than many of the other residues listed in Table 5, especially when compared with those involved in the disulfide linkages

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of 22/87 and 206/216.   Residues 26 and 235 are
absolutely conserved within the Bacillus genus, and
differ only in the thermitase sequence from
Thermoactinomyces.   These residues are decidedly more
hydrophobic than those comprising the disulfide linkages
in subtilisin 7159 and 8307.   It is believed that one
loses more stability from removing hydrophobic residues
from the interior of the protein than one can gain from
the effect of a crosslink on the entropy of the unfolded
state.   The 50/109 linkage may also suffer from this
same problem since only very hydrophobic groups (Met,
Phe, and Trp) are found at this position.

Additional considerations such as these could lead
to an improvement in the probability for selecting
stabilizing disulfide linkages.   Nonetheless, even
without any further modifications of this method, its
success rate for predicting candidate sites on proteins
for the introduction of disulfide linkages is two out of
four or 50%.   No other known method for selecting
disulfide linkages approaches this level of success.
The method of Wetzel (European Patent Appln. 155,832)
has no success in selecting sites when more than one
cysteine needs to be changed.

As an indication of the necessity for the various
steps and rules defined in this present invention, and
also as an insight to how they evolved and were
formulated, it becomes instructive to review examples of
engineered disulfide linkages that failed to stabilize
subtilisin BPN'.   A list of unsuccessful attempts to
engineer disulfide linkages in subtilisin by means
outside the present embodiment of the current invention
is given in Table 6.

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Table 6

Geometry and Homology Parameters for Disulfide Bridge
Sites that Failed to Stabilize Subtilisin BPN'

Residues linked	Strain GX	RMS error	Short M/C	Short S/C	CHI₃	Sequenceᶜ Homology	Effect on Stability
A 1:S 78	7127	0.48	0	0	272	NC	unchanged
A 1:S 78	"	0.54	0	0	252	"	"
S 24:S 87	7123	0.51	2	1	270	NC	unchanged
K 27:S 89	7136	0.71	1	1	239	K27 AC	unchanged
A 85:A232	7122	0.73	-	-	260	A85 AC	decreased
A 85:A232	"	0.73	-	-	83	"	"
I122:V147	7115	0.83	-	-	149	I122 AC	decreased
S249:A273	7124	0.67	-	-	294	A273 AC	decreased
T253:A273	7140	0.29	-	-	93	A273 & T253 AC	decreased
T253:A273	"	0.29	-	-	226	"	"

Of the examples shown in Table 6, all except the
253/273 linkage have RMS values higher than 0.45. This
linkage, which was introduced into subtilisin 7140, has
two residues that are absolutely conserved in the six
sequences given in Table 4. The decreased stability
associated with this protein is believed to be due to
altering important interactions that have been conserved
throughout evolution. Four other proteins, subtilisin
7136, 7122, 7115, and 7124 also contain disulfide
linkages that involve the alteration of a conserved
residue, and all of these, except 7136, have also been
found to have decreased stability relative to the wild-
type protein. These proteins, however, also have the
highest RMS errors, so the reason for the observed
decreased stability is not so apparent in these cases.

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ᶜThe sequence homology is designated as nonconserved
(NC) and absolutely conserved (AC) relative to the six
sequences given in Table 4.

It could derive from a combination of a poor fit (RMS error) and alteration of a conserved interaction.

The two proteins that contain disulfide bridges that are not comprised of conserved residues are subtilisin 7127 and 7123. These linkages also do not have too bad a fit (RMS error of 0.48 and 0.51, respectively). Both proteins were found to have stabilities close to that of the wild-type protein. The failure of the 24/87 linkage to stabilize subtilisin 7123 may be related to the poor short contacts noted in the table. The 1/78 linkage is complex because of the relatively high accessibility of the N-terminus. Complex thiol chemistry which included intermolecular crosslinking was found to occur for subtilisin 7127.

While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth is as follows in the scope of the appended claims.

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WHAT IS CLAIMED IS:

1. A computer based method for evaluating a protein's structure to determine whether said protein contains at least two target amino acid residues, the replacement of at least one of which with a cysteine residue would be sufficient to permit the formation of at least one potentially protein-stabilizing disulfide bridge; said method comprising the steps:

(1) examining each selected pair of amino acid residues in said protein to determine if they contain certain atoms whose relative three-dimensional positions possess a geometric conformation similar to the corresponding atoms of a known disulfide bridge,

(2) examining any pair of amino acids found to contain said certain atoms identified in step (1) to determine whether the new atoms of a possible disulfide linkage can be accommodated without creating unacceptable steric hindrance,

(3) permitting an expert operator (i) to view any possible sites for novel disulfide linkage which can be accommodated without altering the tertiary conformation of said protein molecule, and (ii) to rank said viewed possible sites for a novel disulfide linkage from most likely to stabilize an engineered protein, to least likely to stabilize said protein, and

(4) evaluating said ranked possible sites for a novel disulfide linkage according to expert rule criterion.

2. The computer based method of claim 1 wherein said step (1) further comprises the steps:

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(a) examining the centers-of-mass between the pyramids formed by the main-chain nitrogen, the alpha carbon, the beta carbon and the carbonyl carbon of each of the two amino acids of the selected pair, and

(b) examining the structure of the eight atoms of the pyramids of the two amino acids of the selected pair as a single 8-atom group.

3.   The computer based method of claim 2 wherein said step (1) further comprises the step of determining whether the distance between the centers-of-mass of the two pyramids is (i) less than the largest distance between the centers-of-mass of two cysteine residues in any known disulfide bond, and (ii) greater than the smallest distance between the centers-of-mass of two cysteine residues in any known disulfide bond.

4.   The computer based method of claim 2 wherein said step (1) further comprises comparing the structure of said 8-atom group to each of the different known disulfide linkages.

5.   The computer based method of claim 4 wherein said comparison is performed according to a statistical method.

6.   The computer based method of claim 2 wherein the root mean square (RMS) error and the fit of the selected amino acid pair as compared to each different disulfide bond is recorded in computer memory.

7.   The computer based method of claim 6 wherein the selected amino acid pair is recorded as having

passed step (1) if the RMS error falls below a preset limit.

8. The computer based method of claim 2 wherein an external record is provided which indicates any amino acid pair which passed step (1); said record containing the identities of the amino acid pairs, the identities of the disulfide bond containing the similar geometry, the RMS error of the analysis, and the value of CHI_3 of the fit.

9. The computer based method of claim 7 wherein the selected amino acid pair is discarded if the RMS error exceeds a preset limit and a second amino acid pair is selected for examination.

10. The computer based method of claim 1 wherein step (2) further comprises the step of:

(a) positioning said possible disulfide linkage according to the cystine which best matched the position of said known disulfide bridge of step (1).

(b) calculating the distance between the cysteine residues of said possible disulfide linkage and all nearby atoms, and

(c) recording all distances shorter than a physically reasonable preset value as a short contact.

11. The computer based method of claim 10 wherein step (2) further comprises the step of separately recording (i) the short contacts between said cystine residues and nearby atoms which are main-chain atoms and (ii) the short contacts between said cystine residues and nearby atoms which are side-chain atoms.

12.   The computer based method of claim 11 wherein
step (2) further comprises the step of rejecting any
possible disulfide bridge whose number of short contacts
exceeds a preselected value.

13.   The computer based method of claim 11 which
further comprises the step of providing the number and
kind of short contacts to a user.

14.   The computer based method of claim 11 wherein
each selected pair found to have said certain atoms in
step (1) is ordered first according to the number of
main-chain short contacts, and ordered second according
to the number of side-chain short contacts.

15.   The computer based method of claim 1 wherein
in step (3)(i) the possible disulfide linkage is
displayed using interactive computer graphics.

16.   The computer based method of claim 15 wherein
said computer graphics provides a three-dimensional
representation of said possible disulfide bond.

17.   The computer based method of claim 16 wherein
said computer graphics provides user initiated
functions, said functions selected from the group
comprising: (1) zoom capacity, (2) clipping capacity,
(3) intensity depth queuing, (4) translation capacity,
(5) rotation capacity, (6) on/off control of the logical
segments of the picture, (7) capacity to select atoms in
the most detailed logical segment, and (8) capacity to
control color.

18. The computer based method of claim 1 wherein said expert rule criteria of step (4) comprises the steps:

(a) evaluating possible disulfide linkages to determine whether the formation of said linkages would require the loss of an evolutionally conserved amino acid residue, or

(b) evaluating possible disulfide linkages to determine whether the formation of said linkage would result in the loss of a favorable hydrophobic interaction.

19. The computer based method of claim 18 wherein said step (a) comprises ranking said possible disulfide linkages from most favorable to least favorable based upon the number of conserved amino acid residues which would be lost due to said linkage, wherein the loss of no conserved residues would be most favorable, and the loss of two conserved residues would be least favorable.

20. A computer apparatus, which comprises a processor means comprising:

(a) first means for selecting a first candidate target amino acid residue of a protein

(b) second means for selecting a second candidate target amino acid residue of said protein

(c) means for calculating the error obtained when a known disulfide bond is superimposed on said two candidate target amino acid residues of said protein.

21. The method of claim 20 wherein said error calculated in step (c) is the RMS error and wherein said

disulfide bond is superimposed on said candidate target amino acid residues by the method of least squares.

22.   The computer apparatus of claim 20 which additionally comprises a display means connected to said processor means, said display means comprising a means for displaying to a user upon command the possible disulfide bond between said cysteine residues, whereby computer-designed protein molecules can be displayed.

23.   The computer apparatus of claim 20, wherein:
        said processor means includes a central processing unit, a storage device, an operating system, and application software; and
        said display means includes a visual display monitor, an input device, a storage device, a local processor, and display application software.
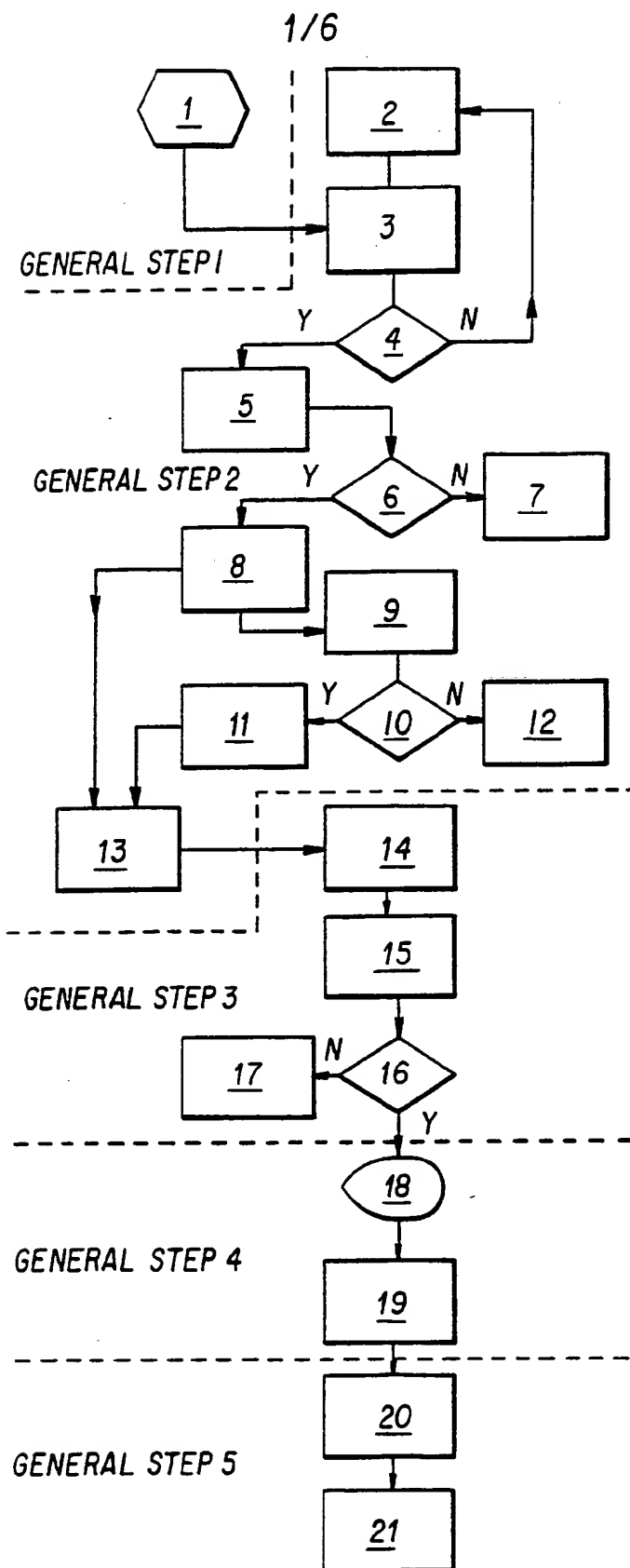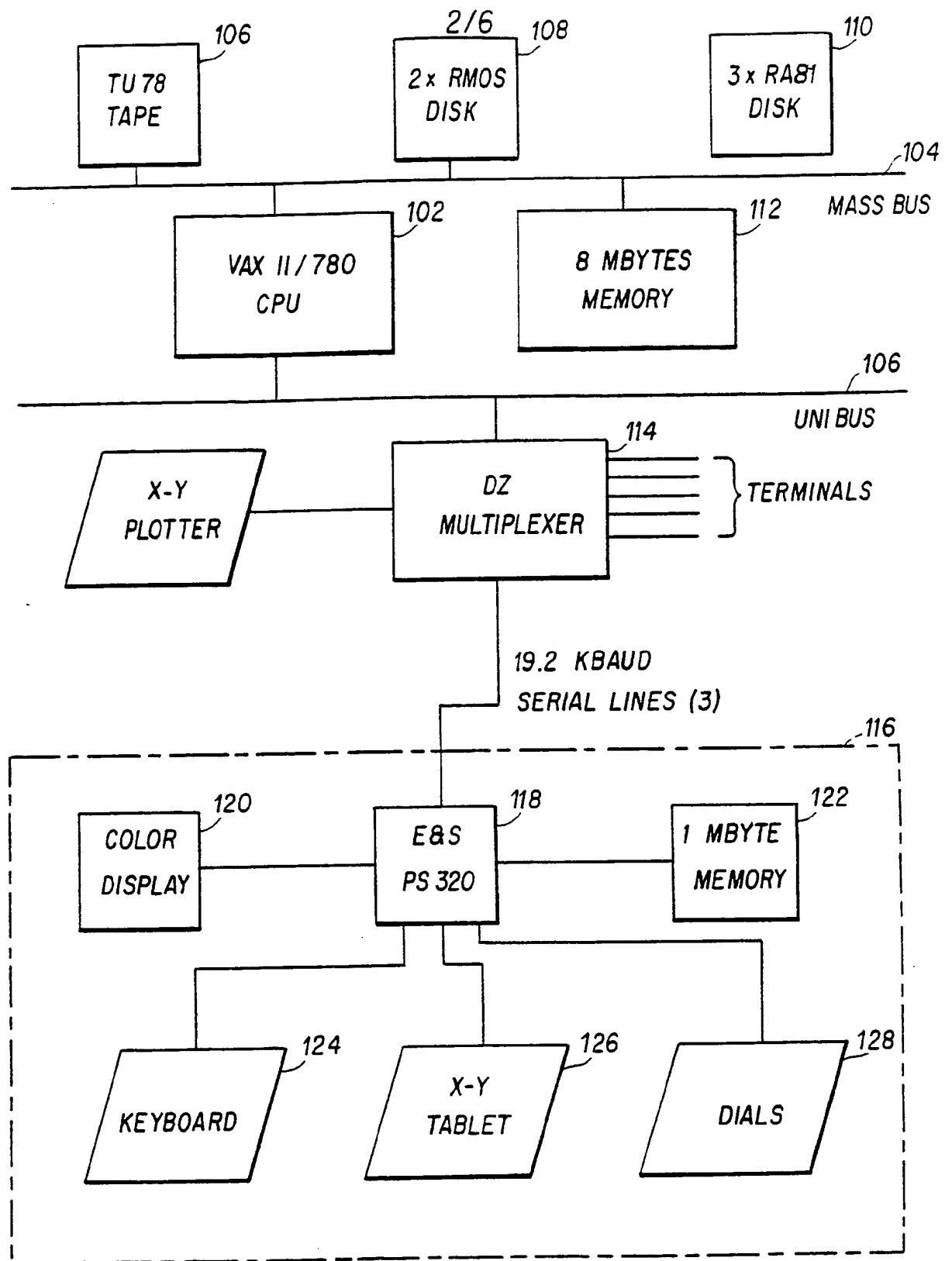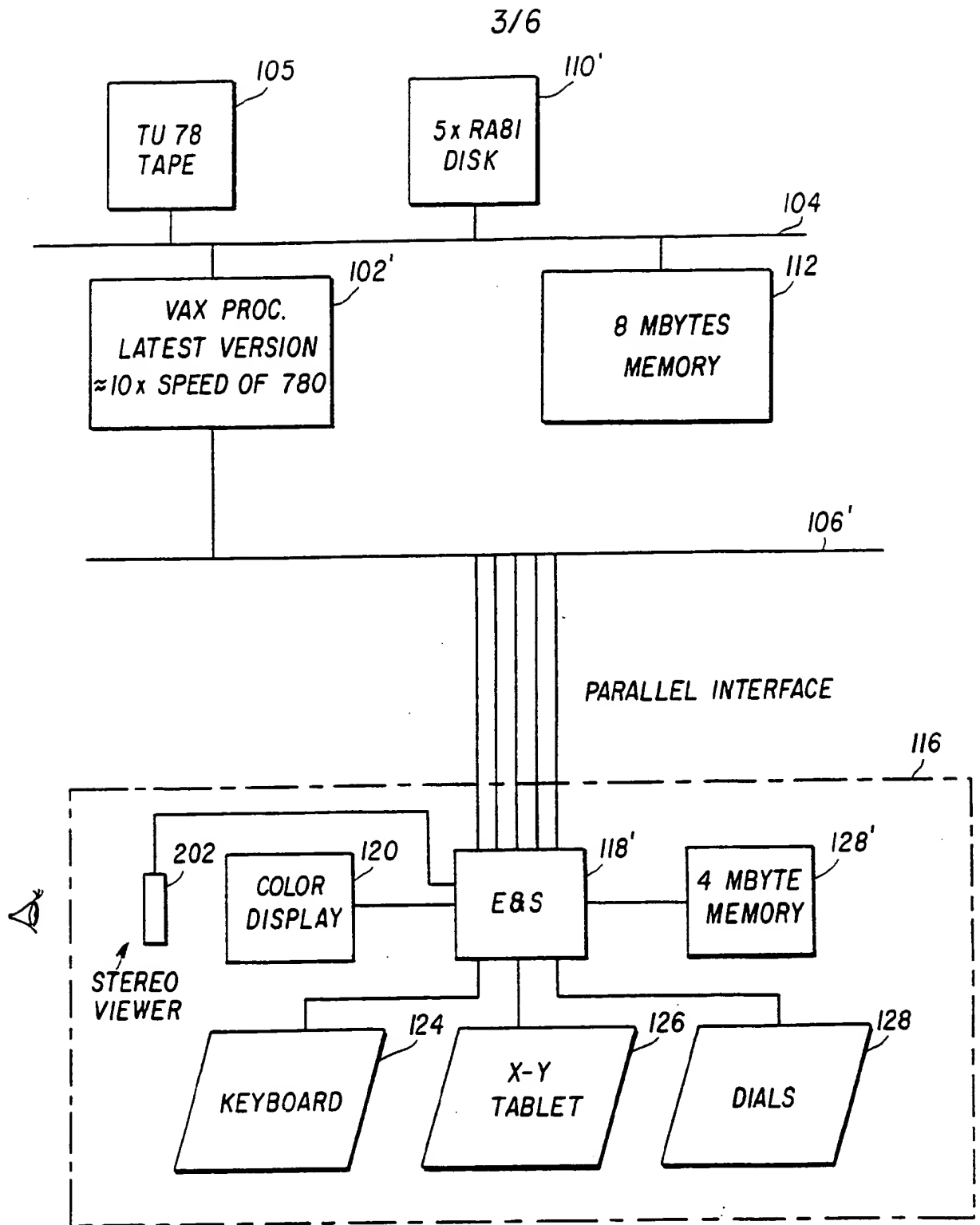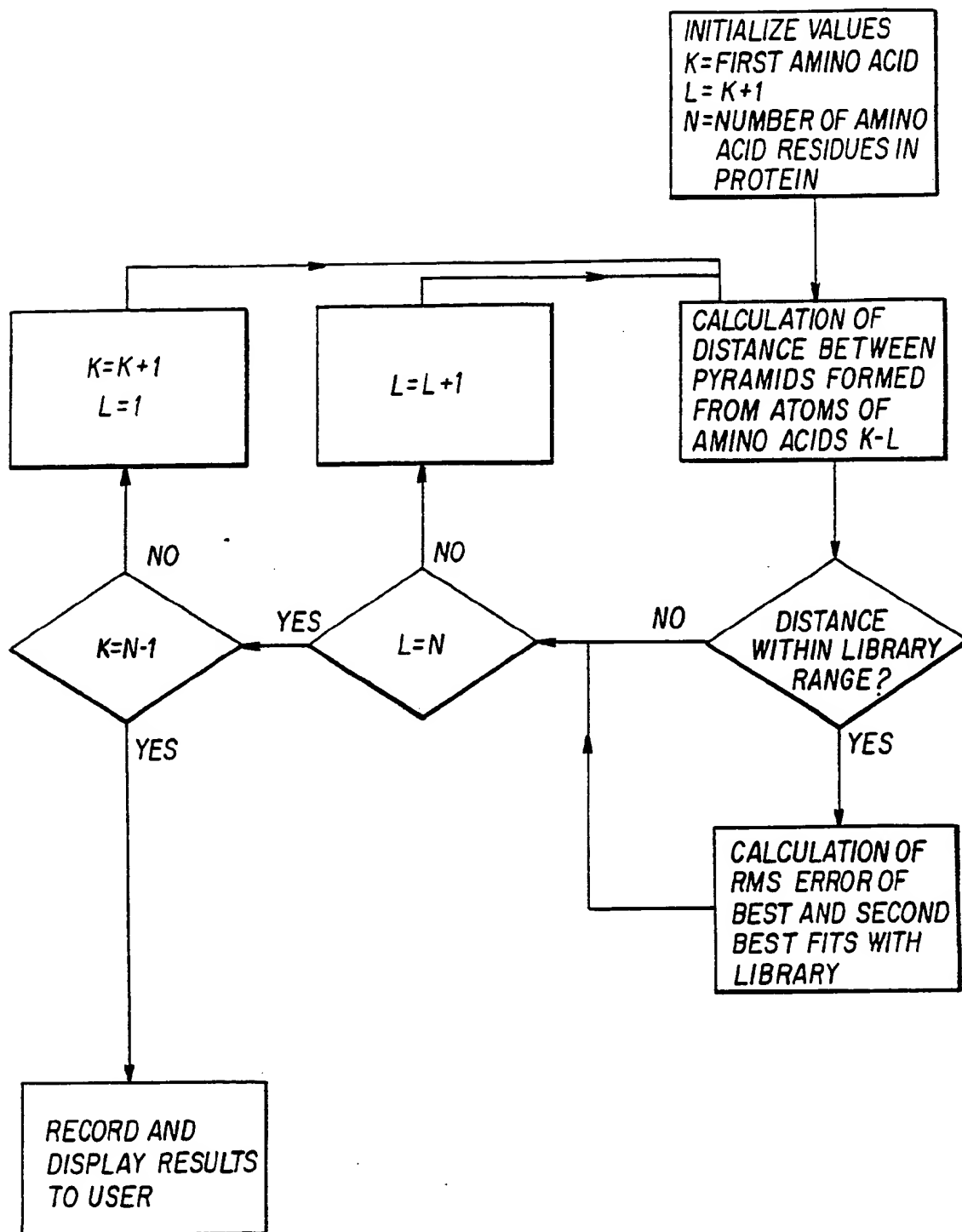
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FIG. I

FIG.2

FIG.3

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INITIALIZE VALUES
K=FIRST AMINO ACID
L = K+1
N=NUMBER OF AMINO
ACID RESIDUES IN
PROTEIN

K=K+1
L=1

L=L+1

CALCULATION OF
DISTANCE BETWEEN
PYRAMIDS FORMED
FROM ATOMS OF
AMINO ACIDS K-L

NO

NO

YES

NO

K=N-1

L=N

DISTANCE
WITHIN LIBRARY
RANGE?

YES

YES

CALCULATION OF
RMS ERROR OF
BEST AND SECOND
BEST FITS WITH
LIBRARY

RECORD AND
DISPLAY RESULTS
TO USER

FIG. 4

```
6000        DO (K=1, (Number of amino acids)-1 )
6010        .   LOCATE_STANDARD_PYRAMID_AT_AMINO_ACID_K
6020        .   IF(Location successful)
6030        .   .   DO (L=K+1,(Number of amino acids))
6040        .   .   .   LOCATE_STANDARD_PYRAMID_AT_AMINO_ACID_L
6050        .   .   .   IF(Location successful)
6060        .   .   .   .   CALCULATE_DISTANCE_BETWEEN_PYRAMIDS
6070        .   .   .   .   IF(distance within bounds)
6080        .   .   .   .   .   DO (Jcys =1,Number_observed_cystines)
6090        .   .   .   .   .   .   CALCULATE_RMS_ERROR_VS_K:L
6100        .   .   .   .   .   .   CALCULATE_RMS_ERROR_VS_L:K
6110        .   .   .   .   .   END_DO (Jcys = 1,....
6120        .   .   .   .   .   FIND_CASE_WITH_SMALLEST_RMS_ERROR
6130        .   .   .   .   .   IF(RMS_error below threshold)
6140        .   .   .   .   .   .   WRITE_EXTERNAL_RECORD
6150        .   .   .   .   .   .   SEARCH_FOR_SECOND_BEST_RMS_ERROR
6160        .   .   .   .   .   .   IF(RMS_error below threshold)
6170        .   .   .   .   .   .   .   WRITE_EXTERNAL_RECORD
6180        .   .   .   .   .   .   END_IF(RMS_e.....
6190        .   .   .   .   .   END_IF(RMS_e.....
6200        .   .   .   .   END_IF(dista......
6210        .   .   .   END_IF(Locat.....
6220        .   .   END_DO (L=K+1,...
6230        .   END_IF(Locati...
6240        END_DO (K=1, (Nu....
```

FIG. 5

```
7000    TO LOCATE_STANDARD_PYRAMID_AT_AMINO_ACID_x
7010    .  IF(Amino acid x is a glycine)
7020    .  .  USE_N_CA_C_TO_ADD_CB
7030    .  END_IF glycine
7040    .  IF(too many atoms missing from model)
7042    .  .  location unsuccessful
7044    .  END_IF(too many ....
7050    .  ELSE
7060    .  .  LEAST_SQUARES_FIT_N_CA_CB_C_TO_STANDARD_PYRAMID
7070    .  .  location successful if RMS_error = 0.2A
7080    .  END_ELSE (= all atoms present in model)
7090    END_(TO LOCATE_STANDARD_PYRAMID_AT_AMINO_ACID_x)
```

FIG.6

```
8000    TO CALCULATE_DISTANCE_BETWEEN_PYRAMIDS
8010    .  FIND_CENTER_OF_MASS_OF_PYRAMID_K
8020    .  FIND_CENTER_OF_MASS_OF_PYRAMID_L
8030    .  distance = separation(centers-of-mass)
8040    END_(TO CALCULATE_DISTANCE_BETWEEN_PYRAMIDS)
```
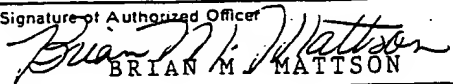
FIG.7

```
9000    TO CALCULATE_RMS_ERROR_VS_pyr#1:pyr#2
9010    .  (N,CA,CB,C) of pyr#1 into slots 1,2,3,4
9020    .  (N,CA,CB,C) of pyr#2 into slots 5,6,7,8
9030    .  LEAST_SQUARES_FIT_EIGHT_ATOMS_TO_CYSTINE_#Jcys
9040    .  REPORT_RMS_ERROR
9050    END_(TO CALCULATE_RMS_ERROR_VS_pyr#1:pyr#2)
```

FIG.8

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US88/00850

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) 6

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC(4): G06F 15/46, G01N 33/00
U.S. Cl.: 364/498, 436/89

II. FIELDS SEARCHED

Minimum Documentation Searched 7

Classification System	Classification Symbols
U.S.	364/496, 497, 498, 500; 436/88, 89, 90

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched 8

III. DOCUMENTS CONSIDERED TO BE RELEVANT 9

Category *	Citation of Document, 11 with indication, where appropriate, of the relevant passages 12	Relevant to Claim No. 13
Y,P	US, A, 4,704,692 (Ladner) 03 November 1987 Column 9, lines 67-68; column 10, lines 1-68; column 11, lines 1-28; column 12, lines 4-68	20-23
A,P	US, A, 4,719,582 (Ishida et al) 12 January 1988 See the entire document.	1-23

* Special categories of cited documents: 10

"A" document defining the general state of the art which is not considered to be of particular relevance

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
03 MAY 1988	27 MAY 1988
International Searching Authority	Signature of Authorized Officer
ISA/US	BRIAN M. MATTSON

Form PCT/ISA/210 (second sheet) (Rev.11-87)

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